

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7 :

C12N 15/54, 9/10, 5/10, 15/89

A2

(11) International Publication Number:

WO 00/09706

(43) International Publication Date:

24 February 2000 (24.02.00)

(21) International Application Number: PCT/US99/18760

(22) International Filing Date: 16 August 1999 (16.08.99)

(30) Priority Data:

60/096,822

17 August 1998 (17.08.98)

US

(71) Applicant (for all designated States except US): PIONEER
HI-BRED INTERNATIONAL, INC. [US/US]; 800 Capital
Square, 400 Locust Street, Des Moines, IA 50309 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): DHUGGA, Kanwarpal,
S. [US/US]; 8320 Barnham Drive, Johnston, IA 50131
(US). HELENTJARIS, Timothy, G. [US/US]; 2960 N.W.
73rd Lane, Ankeny, IA 50021 (US). BOWEN, Benjamin,
A. [GB/US]; 7027 Buckingham Boulevard, Berkeley, CA
94705 (US). WANG, Xun [CN/US]; 12524 Caminito Vista
Soledad, San Diego, CA 92130 (US).(74) Agents: BLAIR, Debra, L. et al.; 7100 N.W. 62nd Avenue,
Darwin Building, Johnston, IA 50131-1000 (US).(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG,
BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB,
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP,
KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,
MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA,
ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ,
UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI
patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR,
NE, SN, TD, TG).

Published

Without international search report and to be republished
upon receipt of that report.

(54) Title: MAIZE CELLULOSE SYNTHASES AND USES THEREOF

(57) Abstract

The invention provides isolated cellulose synthase nucleic acids and their encoded proteins. The present invention provides methods and compositions relating to altering cellulose synthase concentration and/or composition of plants. The invention further provides recombinant expression cassettes, host cells, and transgenic plants.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

Maize Cellulose Synthases and Uses Thereof

TECHNICAL FIELD

The present invention relates generally to plant molecular biology. More specifically, it relates to nucleic acids and methods for modulating their expression in plants.

BACKGROUND OF THE INVENTION

Polysaccharides constitute the bulk of the plant cell walls and have been traditionally classified into three categories: cellulose, hemicellulose, and pectin. Fry, S. C. (1988), *The growing plant cell wall: Chemical and metabolic analysis*. New York: Longman Scientific & Technical. Whereas cellulose is made at the plasma membrane and directly laid down into the cell wall, hemicellulosic and pectic polymers are first made in the Golgi apparatus and then exported to the cell wall by exocytosis. Ray, P. M., *et al.*, (1976), *Ber. Deutsch. Bot. Ges. Bd.* 89, 121-146. The variety of chemical linkages in the pectic and hemicellulosic polysaccharides indicates that there must be tens of polysaccharide synthases in the Golgi apparatus. Darvill *et al.*, (1980). *The primary cell walls of flowering plants*. In *The Plant Cell* (N. E. Tolbert, ed.), *Vol. 1 in Series: The biochemistry of plants: A comprehensive treatise*, eds. P.K. Stumpf and E.E. Conn (New York: Academic Press), pp. 91-162.

Cellulose, by virtue of its ability to form semicrystalline microfibrils, has a very high tensile strength which approaches that of some metals. Niklas, K. J. (1992). *Plant Biomechanics: An engineering approach to plant form and function*, The University of Chicago Press, pp. 607. Bending strength of the culm of normal and brittle-culm mutants of barley has been found to be directly correlated with the concentration of cellulose in the cell wall. Kokubo, *et al.*, (1989), *Plant Physiology* 91, 876-882; Kokubo, *et al.*, (1991) *Plant Physiology* 97, 509-514.

Even though sugar and polysaccharide compositions of the plant cell walls have been well characterized, very limited progress has been made toward identification of the enzymes involved in polysaccharides formation, the reason being their labile nature and recalcitrance to solubilization by available detergents. Sporadic claims for the identification of cellulose synthase from plant sources have been made over the years. Callaghan, T., and Benziman, M. (1984), *Nature* 311, 165-167; Okuda, *et al.*, (1993),

Plant Physiol. 101, 1131-1142. However, these claims have been met with skepticism. Callaghan, T., and Benziman, M. (1985), *Nature* 314, 383-384; Delmer, *et al.*, (1993), Plant Physiol. 103, 307-308. It was only recently that a putative gene for plant cellulose synthase (CelA) was cloned from the developing cotton fibers based on homology to the bacterial gene. Pear, *et al.*, *Proc. Natl. Acad. Sci. (USA)* 93, 12637-12642; Saxena, *et al.*, (1990), *Plant Molecular Biology* 15, 673-684; see also, WO 9818949.

As brittle snap is a major problem in corn breeding, what is needed in the art are compositions and methods for manipulating cellulose concentration in the cell wall and thereby altering plant stalk quality for improved standability or silage. The present invention provides these and other advantages.

SUMMARY OF THE INVENTION

Generally, it is the object of the present invention to provide nucleic acids and proteins relating to cellulose synthases. It is an object of the present invention to provide: 1) nucleic acids and proteins relating to maize cellulose synthases; 2) transgenic plants comprising the nucleic acids of the present invention; 3) methods for modulating, in a transgenic plant, the expression of the nucleic acids of the present invention.

Therefore, in one aspect, the present invention relates to an isolated nucleic acid comprising a member selected from the group consisting of (a) a polynucleotide having a specified sequence identity to a polynucleotide encoding a polypeptide of the present invention;; (b) a polynucleotide which is complementary to the polynucleotide of (a); and (c) a polynucleotide comprising a specified number of contiguous nucleotides from a polynucleotide of (a) or (b). The isolated nucleic acid can be DNA or RNA.

In another aspect, the present invention relates to recombinant expression cassettes, comprising a nucleic acid of the present invention operably linked to a promoter. In some embodiments, the nucleic acid is operably linked in antisense orientation to the promoter.

In another aspect, the present invention is directed to a host cell transfected with the recombinant expression cassette.

In a further aspect, the present invention relates to an isolated protein comprising a polypeptide having a specified number of contiguous amino acids encoded by an isolated nucleic acid of the present invention.

In another aspect, the present invention relates to an isolated nucleic acid comprising a polynucleotide of specified length which selectively hybridizes under stringent conditions to a polynucleotide of the present invention, or a complement thereof. In some embodiments, the isolated nucleic acid is operably linked to a promoter.

In yet another aspect, the present invention relates to an isolated nucleic acid comprising a polynucleotide, the polynucleotide having a specified sequence identity to an identical length of a nucleic acid of the present invention or a complement thereof.

In another aspect, the present invention relates to an isolated nucleic acid comprising a polynucleotide having a sequence of a nucleic acid amplified from a *Zea mays* nucleic acid library using at least two primers or their complements, one of which selectively hybridizes under stringent conditions to a locus of the nucleic acid comprising the 5' terminal coding region and the other primer selectively hybridizing, under stringent conditions, to a locus of the nucleic acid comprising the 3' terminal coding region, and wherein both primers selectively hybridize within the coding region. In some embodiments, the nucleic acid library is a cDNA library.

In another aspect, the present invention relates to a recombinant expression cassette comprising a nucleic acid, wherein the nucleic acid is operably linked to a promoter. In some embodiments, the present invention relates to a host cell transfected with this recombinant expression cassette. In some embodiments, the present invention relates to a protein of the present invention which is produced from this host cell.

In a further aspect, the present invention relates to a heterologous promoter operably linked to a non-isolated polynucleotide of the present invention, wherein the polypeptide is encoded by a nucleic acid amplified from a nucleic acid library.

In yet another aspect, the present invention relates to a transgenic plant comprising a recombinant expression cassette comprising a plant promoter operably linked to any of the isolated nucleic acids of the present invention. In some embodiments, the transgenic plant is *Zea mays*. The present invention also provides transgenic seed from the transgenic plant.

In a further aspect, the present invention relates to a method of modulating expression of the genes encoding the proteins of the present invention in a plant cell capable of plant regeneration, comprising the steps of (a) transforming a plant cell with a recombinant expression cassette comprising a polynucleotide of the present invention

operably linked to a promoter; (b) growing the plant cell under plant growing conditions; and (c) inducing expression of the polynucleotide for a time sufficient to modulate expression of the genes in the plant. In some embodiments, the plant is maize. Expression of the genes encoding the proteins of the present invention can be increased
5 or decreased relative to a non-transformed control plant.

Definitions

Units, prefixes, and symbols may be denoted in their SI accepted form. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino
10 acid sequences are written left to right in amino to carboxy orientation, respectively. Numeric ranges are inclusive of the numbers defining the range and include each integer within the defined range. Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be
15 referred to by their commonly accepted single-letter codes. Unless otherwise provided for, software, electrical, and electronics terms as used herein are as defined in The New IEEE Standard Dictionary of Electrical and electronics Terms (5th edition, 1993). The terms defined below are more fully defined by reference to the specification as a whole.

By "amplified" is meant the construction of multiple copies of a nucleic acid
20 sequence or multiple copies complementary to the nucleic acid sequence using at least one of the nucleic acid sequences as a template. Amplification systems include the polymerase chain reaction (PCR) system, ligase chain reaction (LCR) system, nucleic acid sequence based amplification (NASBA, Cangene, Mississauga, Ontario), Q-Beta Replicase systems, transcription-based amplification system (TAS), and strand
25 displacement amplification (SDA). See, e.g., *Diagnostic Molecular Microbiology: Principles and Applications*, D. H. Persing *et al.*, Ed., American Society for Microbiology, Washington, D.C. (1993). The product of amplification is termed an amplicon.

The term "antibody" includes reference to antigen binding forms of antibodies
30 (e.g., Fab, F(ab)₂). The term "antibody" frequently refers to a polypeptide substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments thereof which specifically bind and recognize an analyte (antigen). However, while various antibody fragments can be defined in terms of the digestion of an intact antibody, one of

skill will appreciate that such fragments may be synthesized *de novo* either chemically or by utilizing recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments such as single chain Fv, chimeric antibodies (i.e., comprising constant and variable regions from different species), humanized antibodies (i.e., comprising a complementarity determining region (CDR) from a non-human source) and heteroconjugate antibodies (e.g., bispecific antibodies).

The term "antigen" includes reference to a substance to which an antibody can be generated and/or to which the antibody is specifically immunoreactive. The specific immunoreactive sites within the antigen are known as epitopes or antigenic determinants. These epitopes can be a linear array of monomers in a polymeric composition - such as amino acids in a protein - or consist of or comprise a more complex secondary or tertiary structure. Those of skill will recognize that all immunogens (i.e., substances capable of eliciting an immune response) are antigens; however some antigens, such as haptens, are not immunogens but may be made immunogenic by coupling to a carrier molecule. An antibody immunologically reactive with a particular antigen can be generated *in vivo* or by recombinant methods such as selection of libraries of recombinant antibodies in phage or similar vectors. See, e.g., Huse *et al.*, *Science* 246: 1275-1281 (1989); and Ward, *et al.*, *Nature* 341: 544-546 (1989); and Vaughan *et al.*, *Nature Biotech.* 14: 309-314 (1996).

As used herein, "antisense orientation" includes reference to a duplex polynucleotide sequence which is operably linked to a promoter in an orientation where the antisense strand is transcribed. The antisense strand is sufficiently complementary to an endogenous transcription product such that translation of the endogenous transcription product is often inhibited.

As used herein, "chromosomal region" includes reference to a length of a chromosome which may be measured by reference to the linear segment of DNA which it comprises. The chromosomal region can be defined by reference to two unique DNA sequences, i.e., markers.

The term "conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or conservatively modified variants of the amino acid sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations" and represent one
5 species of conservatively modified variation. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of ordinary skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine; and UGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule.
10 Accordingly, each silent variation of a nucleic acid which encodes a polypeptide of the present invention is implicit in each described polypeptide sequence and incorporated herein by reference.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein
15 sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Thus, any number of amino acid residues selected from the group of integers consisting of from 1 to 15 can be so altered. Thus, for example, 1, 2, 3, 4, 5, 7, or 10
20 alterations can be made. Conservatively modified variants typically provide similar biological activity as the unmodified polypeptide sequence from which they are derived. For example, substrate specificity, enzyme activity, or ligand/receptor binding is generally at least 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the native protein for its native substrate. Conservative substitution tables providing functionally similar
25 amino acids are well known in the art.

The following six groups each contain amino acids that are conservative substitutions for one another:

- 1) Alanine (A), Serine (S), Threonine (T);
- 2) Aspartic acid (D), Glutamic acid (E);
- 30 3) Asparagine (N), Glutamine (Q);
- 4) Arginine (R), Lysine (K);
- 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and
- 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

See also, Creighton (1984) Proteins W.H. Freeman and Company.

By "encoding" or "encoded", with respect to a specified nucleic acid, is meant comprising the information for translation into the specified protein. A nucleic acid encoding a protein may comprise non-translated sequences (e.g., introns) within
5 translated regions of the nucleic acid, or may lack such intervening non-translated sequences (e.g., as in cDNA). The information by which a protein is encoded is specified by the use of codons. Typically, the amino acid sequence is encoded by the nucleic acid using the "universal" genetic code. However, variants of the universal code, such as are present in some plant, animal, and fungal mitochondria, the bacterium
10 *Mycoplasma capricolum* (*Proc. Natl. Acad. Sci. (USA)*, 82: 2306-2309 (1985)), or the ciliate *Macronucleus*, may be used when the nucleic acid is expressed using these organisms.

When the nucleic acid is prepared or altered synthetically, advantage can be taken of known codon preferences of the intended host where the nucleic acid is to be
15 expressed. For example, although nucleic acid sequences of the present invention may be expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray *et al.* *Nucl. Acids Res.* 17: 477-498 (1989)). Thus, the maize preferred codon for a
20 particular amino acid may be derived from known gene sequences from maize. Maize codon usage for 28 genes from maize plants are listed in Table 4 of Murray *et al.*, *above*.

As used herein "full-length sequence" in reference to a specified polynucleotide or its encoded protein means having the entire amino acid sequence of, a native (non-
25 synthetic), endogenous, catalytically active form of the specified protein. Methods to determine whether a sequence is full-length are well known in the art including such exemplary techniques as northern or western blots, primer extension, S1 protection, and ribonuclease protection. See, e.g., *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997). Comparison to known full-length
30 homologous (orthologous and/or paralogous) sequences can also be used to identify full-length sequences of the present invention. Additionally, consensus sequences typically present at the 5' and 3' untranslated regions of mRNA aid in the identification of a polynucleotide as full-length. For example, the consensus sequence ANNNNAUGG,

where the underlined codon represents the N-terminal methionine, aids in determining whether the polynucleotide has a complete 5' end. Consensus sequences at the 3' end, such as polyadenylation sequences, aid in determining whether the polynucleotide has a complete 3' end.

5 The term "gene activity" refers to one or more steps involved in gene expression, including transcription, translation, and the functioning of the protein encoded by the gene.

 As used herein, "heterologous" in reference to a nucleic acid is a nucleic acid that originates from a foreign species, or, if from the same species, is substantially modified
10 from its native form in composition and/or genomic locus by deliberate human intervention. For example, a promoter operably linked to a heterologous structural gene is from a species different from that from which the structural gene was derived, or, if from the same species, one or both are substantially modified from their original form. A heterologous protein may originate from a foreign species or, if from the same
15 species, is substantially modified from its original form by deliberate human intervention.

 By "host cell" is meant a cell which contains a vector and supports the replication and/or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells.
20 Preferably, host cells are monocotyledonous or dicotyledonous plant cells. A particularly preferred monocotyledonous host cell is a maize host cell.

 The term "hybridization complex" includes reference to a duplex nucleic acid structure formed by two single-stranded nucleic acid sequences selectively hybridized with each other.
25 By "immunologically reactive conditions" or "immunoreactive conditions" is meant conditions which allow an antibody, generated to a particular epitope, to bind to that epitope to a detectably greater degree (e.g., at least 2-fold over background) than the antibody binds to substantially all other epitopes in a reaction mixture comprising the particular epitope. Immunologically reactive conditions are dependent upon the format
30 of the antibody binding reaction and typically are those utilized in immunoassay protocols. See Harlow and Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York (1988), for a description of immunoassay formats and conditions.

The term "introduced" in the context of inserting a nucleic acid into a cell, means "transfection" or "transformation" or "transduction" and includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

The terms "isolated" refers to material, such as a nucleic acid or a protein, which is: (1) substantially or essentially free from components which normally accompany or interact with it as found in its naturally occurring environment. The isolated material optionally comprises material not found with the material in its natural environment; or (2) if the material is in its natural environment, the material has been synthetically (non-naturally) altered by deliberate human intervention to a composition and/or placed at a locus in the cell (e.g., genome or subcellular organelle) not native to a material found in that environment. The alteration to yield the synthetic material can be performed on the material within or removed from its natural state. For example, a naturally occurring nucleic acid becomes an isolated nucleic acid if it is altered, or if it is transcribed from DNA which has been altered, by non-natural, synthetic (i.e., "man-made") methods performed within the cell from which it originates. See, e.g., Compounds and Methods for Site Directed Mutagenesis in Eukaryotic Cells, Kmiec, U.S. Patent No. 5,565,350; *In Vivo* Homologous Sequence Targeting in Eukaryotic Cells; Zarling *et al.*, PCT/US93/03868. Likewise, a naturally occurring nucleic acid (e.g., a promoter) becomes isolated if it is introduced by non-naturally occurring means to a locus of the genome not native to that nucleic acid. Nucleic acids which are "isolated" as defined herein, are also referred to as "heterologous" nucleic acids.

Unless otherwise stated, the term "cellulose synthase nucleic acid" is a nucleic acid of the present invention and means a nucleic acid comprising a polynucleotide of the present invention (a "cellulose synthase polynucleotide") encoding a cellulose synthase polypeptide. A "cellulose synthase gene" is a gene of the present invention and refers to a non-heterologous genomic form of a full-length cellulose synthase polynucleotide.

As used herein, "localized within the chromosomal region defined by and including" with respect to particular markers includes reference to a contiguous length of a chromosome delimited by and including the stated markers.

As used herein, "marker" includes reference to a locus on a chromosome that serves to identify a unique position on the chromosome. A "polymorphic marker" includes reference to a marker which appears in multiple forms (alleles) such that different forms of the marker, when they are present in a homologous pair, allow transmission of each of the chromosomes in that pair to be followed. A genotype may be defined by use of one or a plurality of markers.

As used herein, "nucleic acid" includes reference to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, encompasses known analogues having the essential nature of natural nucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to naturally occurring nucleotides (e.g., peptide nucleic acids).

By "nucleic acid library" is meant a collection of isolated DNA or RNA molecules which comprise and substantially represent the entire transcribed fraction of a genome of a specified organism. Construction of exemplary nucleic acid libraries, such as genomic and cDNA libraries, is taught in standard molecular biology references such as Berger and Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology*, Vol. 152, Academic Press, Inc., San Diego, CA (Berger); Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual*, 2nd ed., Vol. 1-3 (1989); and *Current Protocols in Molecular Biology*, F.M. Ausubel *et al.*, Eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (1994 Supplement).

As used herein "operably linked" includes reference to a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

As used herein, the term "plant" includes reference to whole plants, plant parts or organs (e.g., leaves, stems, roots, etc.), plant cells, seeds and progeny of same. Plant cell, as used herein includes, without limitation, cells obtained from or found in: seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores. Plant cells can also be understood to include modified cells, such as protoplasts, obtained from the aforementioned tissues.

The class of plants which can be used in the methods of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and dicotyledonous plants. Particularly preferred plants include maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
5 millet.

As used herein, "polynucleotide" includes reference to a deoxyribosepolynucleotide, ribopolynucleotide, or analogs thereof that have the essential nature of a natural ribonucleotide in that they hybridize, under stringent hybridization conditions, to substantially the same nucleotide sequence as naturally occurring
10 nucleotides and/or allow translation into the same amino acid(s) as the naturally occurring nucleotide(s). A polynucleotide can be full-length or a subsequence of a native or heterologous structural or regulatory gene. Unless otherwise indicated, the term includes reference to the specified sequence as well as the complementary sequence thereof. Thus, DNAs or RNAs with backbones modified for stability or for other reasons
15 are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term polynucleotide as
20 it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including *among other things*, simple and complex cells.

The terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in
25 which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. The essential nature of such analogues of naturally occurring amino acids is that, when incorporated into a protein, that protein is specifically reactive to antibodies elicited to the same protein but consisting entirely of naturally occurring
30 amino acids. The terms "polypeptide", "peptide" and "protein" are also inclusive of modifications including, but not limited to, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation. Exemplary modifications are described in most basic texts, such as, *Proteins - Structure*

and *Molecular Properties*, 2nd ed., T. E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as, for example, those provided by Wold, F., *Post-translational Protein Modifications: Perspectives and Prospects*, pp. 1-12 in *Posttranslational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter *et al.*, *Meth. Enzymol.* 182: 626-646 (1990) and Rattan *et al.*, *Protein Synthesis: Posttranslational Modifications and Aging*, *Ann. N.Y. Acad. Sci.* 663: 48-62 (1992). It will be appreciated, as is well known and as noted above, that polypeptides are not always entirely linear. For instance, polypeptides may be branched as a result of ubiquitination, and they may be circular, with or without branching, generally as a result of posttranslation events, including natural processing event and events brought about by human manipulation which do not occur naturally. Circular, branched and branched circular polypeptides may be synthesized by non-translation natural process and by entirely synthetic methods, as well. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. In fact, blockage of the amino or carboxyl group in a polypeptide, or both, by a covalent modification, is common in naturally occurring and synthetic polypeptides and such modifications may be present in polypeptides of the present invention, as well. For instance, the amino terminal residue of polypeptides made in *E. coli* or other cells, prior to proteolytic processing, almost invariably will be N-formylmethionine. During post-translational modification of the peptide, a methionine residue at the NH₂-terminus may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionine-less amino terminal variants of the protein of the invention. In general, as used herein, the term polypeptide encompasses all such modifications, particularly those that are present in polypeptides synthesized by expressing a polynucleotide in a host cell.

As used herein "promoter" includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria which comprise genes expressed in plant cells such *Agrobacterium* or *Rhizobium*. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, or seeds. Such promoters are

referred to as "tissue preferred". Promoters which initiate transcription only in certain tissue are referred to as "tissue specific". A "cell type" specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An "inducible" promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters constitute the class of "non-constitutive" promoters. A "constitutive" promoter is a promoter which is active under most environmental conditions.

10 The term "cellulose synthase polypeptide" is a polypeptide of the present invention and refers to one or more amino acid sequences, in glycosylated or non-glycosylated form. The term is also inclusive of fragments, variants, homologs, alleles or precursors (e.g., preproteins or proproteins) thereof. A "cellulose synthase protein" is a protein of the present invention and comprises a cellulose synthase polypeptide.

15 As used herein "recombinant" includes reference to a cell or vector, that has been modified by the introduction of a heterologous nucleic acid or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under-expressed or not expressed at all as a result of deliberate human intervention. The term "recombinant" as used herein does not encompass the alteration of the cell or vector by naturally occurring events (e.g., spontaneous mutation, natural transformation/transduction/transposition) such as those occurring without deliberate human intervention.

20 As used herein, a "recombinant expression cassette" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements which permit transcription of a particular nucleic acid in a host cell. The recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression cassette portion of an expression vector includes, among other sequences, a nucleic acid to be transcribed, and a promoter.

25 The term "residue" or "amino acid residue" or "amino acid" are used interchangeably herein to refer to an amino acid that is incorporated into a protein,

polypeptide, or peptide (collectively "protein"). The amino acid may be a naturally occurring amino acid and, unless otherwise limited, may encompass known analogs of natural amino acids that can function in a similar manner as naturally occurring amino acids.

5 The term "selectively hybridizes" includes reference to hybridization, under stringent hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence to a detectably greater degree (e.g., at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively hybridizing sequences typically have about at least
10 80% sequence identity, preferably 90% sequence identity, and most preferably 100% sequence identity (i.e., complementary) with each other.

 The term "specifically reactive", includes reference to a binding reaction between an antibody and a protein having an epitope recognized by the antigen binding site of the antibody. This binding reaction is determinative of the presence of a protein having the
15 recognized epitope amongst the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to an analyte having the recognized epitope to a substantially greater degree (e.g., at least 2-fold over background) than to substantially all other analytes lacking the epitope which are present in the sample.

20 The terms "stringent conditions" or "stringent hybridization conditions" includes reference to conditions under which a probe will hybridize to its target sequence, to a detectably greater degree than other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing
25 conditions, target sequences can be identified which are 100% complementary to the probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, preferably less than 500 nucleotides in length.

30 Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50

nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, *Anal. Biochem.*, 138:267-284 (1984): $T_m = 81.5\text{ }^{\circ}\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1 °C for each 1% of mismatching; thus, T_m , hybridization and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10 °C. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4 °C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10 °C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20 °C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45 °C (aqueous solution) or 32 °C (formamide solution) it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive

guide to the hybridization of nucleic acids is found in Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays", Elsevier, New York (1993); and *Current Protocols in Molecular Biology*, Chapter 2, Ausubel, *et al.*, Eds., Greene Publishing and Wiley-Interscience, New York (1995).

As used herein, "transgenic plant" includes reference to a plant which comprises within its genome a heterologous polynucleotide. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenics initially so altered as well as those created by sexual crosses or asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

As used herein, "vector" includes reference to a nucleic acid used in transfection of a host cell and into which can be inserted a polynucleotide. Vectors are often replicons. Expression vectors permit transcription of a nucleic acid inserted therein.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" means includes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence may be compared to a reference sequence and wherein the

portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally
5 can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well-known in the art.

10 Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.* 2: 482 (1981); by the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.* 48: 443 (1970); by the search for similarity method of Pearson and Lipman, *Proc. Natl. Acad. Sci.* 85: 2444 (1988); by computerized implementations of these algorithms, including, but not limited
15 to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, California, GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wisconsin, USA; the CLUSTAL program is well described by Higgins and Sharp, *Gene* 73: 237-244 (1988); Higgins and Sharp, *CABIOS* 5: 151-153 (1989); Corpet, *et al.*, *Nucleic
20 Acids Research* 16: 10881-90 (1988); Huang, *et al.*, *Computer Applications in the Biosciences* 8: 155-65 (1992), and Pearson, *et al.*, *Methods in Molecular Biology* 24: 307-331 (1994). The BLAST family of programs which can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database
25 sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, *Current Protocols in Molecular Biology*, Chapter 19, Ausubel, *et al.*, Eds., Greene Publishing and Wiley-Interscience, New York (1995).

30 Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the BLAST 2.0 suite of programs using default parameters. Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402 (1997). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology

Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, $M=5$, $N=-4$, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance.

BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen, *Comput. Chem.*, 17:149-163 (1993)) and

XNU (Claverie and States, *Comput. Chem.*, 17:191-201 (1993)) low-complexity filters can be employed alone or in combination.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences which are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g. charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences which differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., according to the algorithm of Meyers and Miller, *Computer Applic. Biol. Sci.*, 4: 11-17 (1988) e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

(e) (i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70% sequence identity, preferably at least 80%, more preferably at least 90% and most preferably at least 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 60%, more preferably at least 70%, 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. However, nucleic acids which do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This may occur, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is that the polypeptide which the first nucleic acid encodes is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e) (ii) The terms "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70% sequence identity to a reference sequence, preferably 80%, more preferably 85%, most preferably at least 90% or 95% sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.* 48: 443 (1970). An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution. Peptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes.

DETAILED DESCRIPTION OF THE INVENTION

Overview

The present invention provides, *among other things*, compositions and methods for modulating (i.e., increasing or decreasing) the level of polypeptides of the present invention in plants. In particular, the polypeptides of the present invention can
5 be expressed at developmental stages, in tissues, and/or in quantities which are uncharacteristic of non-recombinantly engineered plants. Thus, the present invention provides utility in such exemplary applications as improvement of stalk quality for improved stand or silage. Further, the present invention provides for an increased concentration of cellulose in the pericarp; hardening the kernel and thus improving its
10 handling ability.

The present invention also provides isolated nucleic acid comprising polynucleotides of sufficient length and complementarity to a gene of the present invention to use as probes or amplification primers in the detection, quantitation, or isolation of gene transcripts. For example, isolated nucleic acids of the present invention
15 can be used as probes in detecting deficiencies in the level of mRNA in screenings for desired transgenic plants, for detecting mutations in the gene (e.g., substitutions, deletions, or additions), for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants (polymorphisms) of the gene, or for use as molecular markers in plant breeding
20 programs. The isolated nucleic acids of the present invention can also be used for recombinant expression of their encoded polypeptides, or for use as immunogens in the preparation and/or screening of antibodies. The isolated nucleic acids of the present invention can also be employed for use in sense or antisense suppression of one or more genes of the present invention in a host cell, tissue, or plant. Attachment of chemical
25 agents which bind, intercalate, cleave and/or crosslink to the isolated nucleic acids of the present invention can also be used to modulate transcription or translation.

The present invention also provides isolated proteins comprising a polypeptide of the present invention (e.g., preproenzyme, proenzyme, or enzymes). The present invention also provides proteins comprising at least one epitope from a polypeptide of the
30 present invention. The proteins of the present invention can be employed in assays for enzyme agonists or antagonists of enzyme function, or for use as immunogens or antigens to obtain antibodies specifically immunoreactive with a protein of the present invention. Such antibodies can be used in assays for expression levels, for identifying

and/or isolating nucleic acids of the present invention from expression libraries, or for purification of polypeptides of the present invention.

The isolated nucleic acids and proteins of the present invention can be used over a broad range of plant types, particularly monocots such as the species of the Family

5 *Graminae* including *Sorghum bicolor* and *Zea mays*. The isolated nucleic acid and proteins of the present invention can also be used in species from the genera: *Cucurbita*, *Rosa*, *Vitis*, *Juglans*, *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersicon*, *Nicotiana*, *Solanum*,

10 *Petunia*, *Digitalis*, *Majorana*, *Ciahorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Heterocallis*, *Nemesis*, *Pelargonium*, *Panieum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Pisum*, *Phaseolus*, *Lolium*, *Oryza*, *Avena*, *Hordeum*, *Secale*, *Triticum*, *Bambusa*, *Dendrocalamus*, and *Melocanna*.

15 Nucleic Acids

The present invention provides, *among other things*, isolated nucleic acids of RNA, DNA, and analogs and/or chimeras thereof, comprising a polynucleotide of the present invention.

A polynucleotide of the present invention is inclusive of:

20 (a) a polynucleotide encoding a polypeptide of SEQ ID NOS: 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, and 58, and conservatively modified and polymorphic variants thereof, including exemplary polynucleotides of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57;

(b) a polynucleotide which is the product of amplification from a *Zea mays*

25 nucleic acid library using primer pairs which selectively hybridize under stringent conditions to loci within a polynucleotide selected from the group consisting of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57, wherein the polynucleotide has substantial sequence identity to a polynucleotide selected from the group consisting of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53,

30 and 57;

(c) a polynucleotide which selectively hybridizes to a polynucleotide of (a) or (b);

(d) a polynucleotide having a specified sequence identity with polynucleotides of (a), (b), or (c);

(e) a polynucleotide encoding a protein having a specified number of contiguous amino acids from a prototype polypeptide, wherein the protein is specifically recognized by antisera elicited by presentation of the protein and wherein the protein does not detectably immunoreact to antisera which has been fully immunosorbed with the protein;

5 (f) complementary sequences of polynucleotides of (a), (b), (c), (d), or (e); and

(g) a polynucleotide comprising at least a specific number of contiguous nucleotides from a polynucleotide of (a), (b), (c), (d), (e), or (f).

10 *A. Polynucleotides Encoding A Polypeptide of the Present Invention or Conservatively Modified or Polymorphic Variants Thereof*

As indicated in (a), above, the present invention provides isolated nucleic acids comprising a polynucleotide of the present invention, wherein the polynucleotide encodes a polypeptide of the present invention, or conservatively modified or polymorphic variants thereof. Those of skill in the art will recognize that the degeneracy of the genetic code allows for a plurality of polynucleotides to encode for the identical amino acid sequence. Such "silent variations" can be used, for example, to selectively hybridize and detect allelic variants of polynucleotides of the present invention. Accordingly, the present invention includes polynucleotides of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57, and silent variations of polynucleotides encoding a polypeptide of SEQ ID NOS: 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, and 58. The present invention further provides isolated nucleic acids comprising polynucleotides encoding conservatively modified variants of a polypeptide of SEQ ID NOS: 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, and 58. Additionally, the present invention further provides isolated nucleic acids comprising polynucleotides encoding one or more polymorphic (allelic) variants of polypeptides/polynucleotides. Polymorphic variants are frequently used to follow segregation of chromosomal regions in, for example, marker assisted selection methods for crop improvement.

30

B. Polynucleotides Amplified from a Zea mays Nucleic Acid Library

As indicated in (b), above, the present invention provides an isolated nucleic acid comprising a polynucleotide of the present invention, wherein the polynucleotides are amplified from a *Zea mays* nucleic acid library. *Zea mays* lines B73, PHRE1, A632, BMS-P2#10, W23, and Mo17 are known and publicly available. Other publicly known and available maize lines can be obtained from the Maize Genetics Cooperation (Urbana, IL). The nucleic acid library may be a cDNA library, a genomic library, or a library generally constructed from nuclear transcripts at any stage of intron processing. cDNA libraries can be normalized to increase the representation of relatively rare cDNAs. In optional embodiments, the cDNA library is constructed using a full-length cDNA synthesis method. Examples of such methods include Oligo-Capping (Maruyama, K. and Sugano, S. *Gene* 138: 171-174, 1994), Biotinylated CAP Trapper (Carninci, P., Kvan, C., *et al.* *Genomics* 37: 327-336, 1996), and CAP Retention Procedure (Edery, E., Chu, L.L., *et al.* *Molecular and Cellular Biology* 15: 3363-3371, 1995). cDNA synthesis is often catalyzed at 50-55°C to prevent formation of RNA secondary structure. Examples of reverse transcriptases that are relatively stable at these temperatures are SuperScript II Reverse Transcriptase (Life Technologies, Inc.), AMV Reverse Transcriptase (Boehringer Mannheim) and RetroAmp Reverse Transcriptase (Epicentre). Rapidly growing tissues, or rapidly dividing cells are preferably used as mRNA sources such as from the elongating internode of corn plants.

The polynucleotides of the present invention include those amplified using the following primer pairs:

SEQ ID NOS: 3 and 4 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 1;

SEQ ID NOS: 7 and 8 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 5; and

SEQ ID NOS: 11 and 12 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 9.

SEQ ID NOS: 15 and 16 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 13.

SEQ ID NOS: 19 and 20 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 17;

SEQ ID NOS: 23 and 24 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 21; and

SEQ ID NOS: 27 and 28 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 25.

5 SEQ ID NOS: 31 and 32 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 29.

SEQ ID NOS: 35 and 36 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 33;

10 SEQ ID NOS: 39 and 40 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 37; and

SEQ ID NOS: 43 and 44 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 41.

SEQ ID NOS: 47 and 48 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 45.

15 SEQ ID NOS: 51 and 52 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 49;

SEQ ID NOS: 55 and 56 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 53; and

20 SEQ ID NOS: 59 and 60 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NO: 57.

The present invention also provides subsequences of the polynucleotides of the present invention. A variety of subsequences can be obtained using primers which selectively hybridize under stringent conditions to at least two sites within a polynucleotide of the present invention, or to two sites within the nucleic acid which
25 flank and comprise a polynucleotide of the present invention, or to a site within a polynucleotide of the present invention and a site within the nucleic acid which comprises it. Primers are chosen to selectively hybridize, under stringent hybridization conditions, to a polynucleotide of the present invention. Generally, the primers are complementary to a subsequence of the target nucleic acid which they amplify. As those
30 skilled in the art will appreciate, the sites to which the primer pairs will selectively hybridize are chosen such that a single contiguous nucleic acid can be formed under the desired amplification conditions.

In optional embodiments, the primers will be constructed so that they selectively hybridize under stringent conditions to a sequence (or its complement) within the target nucleic acid which comprises the codon encoding the carboxy or amino terminal amino acid residue (i.e., the 3' terminal coding region and 5' terminal coding region, respectively) of the polynucleotides of the present invention. Optionally within these 5 embodiments, the primers will be constructed to selectively hybridize entirely within the coding region of the target polynucleotide of the present invention such that the product of amplification of a cDNA target will consist of the coding region of that cDNA. The primer length in nucleotides is selected from the group of integers consisting of from at 10 least 15 to 50. Thus, the primers can be at least 15, 18, 20, 25, 30, 40, or 50 nucleotides in length. Those of skill will recognize that a lengthened primer sequence can be employed to increase specificity of binding (i.e., annealing) to a target sequence. A non-annealing sequence at the 5' end of a primer (a "tail") can be added, for example, to introduce a cloning site at the terminal ends of the amplicon.

15 The amplification products can be translated using expression systems well known to those of skill in the art and as discussed, *infra*. The resulting translation products can be confirmed as polypeptides of the present invention by, for example, assaying for the appropriate catalytic activity (e.g., specific activity and/or substrate specificity), or verifying the presence of one or more linear epitopes which are specific 20 to a polypeptide of the present invention. Methods for protein synthesis from PCR derived templates are known in the art and available commercially. See, e.g., Amersham Life Sciences, Inc, Catalog '97, p.354.

Methods for obtaining 5' and/or 3' ends of a vector insert are well known in the art. See, e.g., RACE (Rapid Amplification of Complementary Ends) as described in 25 Frohman, M. A., in PCR Protocols: A Guide to Methods and Applications, M. A. Innis, D. H. Gelfand, J. J. Sninsky, T. J. White, Eds. (Academic Press, Inc., San Diego, 1990), pp. 28-38.; see also, U.S. Pat. No. 5,470,722, and *Current Protocols in Molecular Biology*, Unit 15.6, Ausubel, *et al.*, Eds., Greene Publishing and Wiley-Interscience, New York (1995); Frohman and Martin, *Techniques* 1:165 (1989).

30

C. Polynucleotides Which Selectively Hybridize to a Polynucleotide of (A) or (B)

As indicated in (c), above, the present invention provides isolated nucleic acids comprising polynucleotides of the present invention, wherein the polynucleotides

selectively hybridize, under selective hybridization conditions, to a polynucleotide of paragraphs (A) or (B) as discussed, *above*. Thus, the polynucleotides of this embodiment can be used for isolating, detecting, and/or quantifying nucleic acids comprising the polynucleotides of (A) or (B). For example, polynucleotides of the present invention can be used to identify, isolate, or amplify partial or full-length clones in a deposited library. In some embodiments, the polynucleotides are genomic or cDNA sequences isolated or otherwise complementary to a cDNA from a dicot or monocot nucleic acid library. Exemplary species of monocots and dicots include, but are not limited to: corn, canola, soybean, cotton, wheat, sorghum, sunflower, oats, sugar cane, millet, barley, and rice. Optionally, the cDNA library comprises at least 80% full-length sequences, preferably at least 85% or 90% full-length sequences, and more preferably at least 95% full-length sequences. The cDNA libraries can be normalized to increase the representation of rare sequences. Low stringency hybridization conditions are typically, but not exclusively, employed with sequences having a reduced sequence identity relative to complementary sequences. Moderate and high stringency conditions can optionally be employed for sequences of greater identity. Low stringency conditions allow selective hybridization of sequences having about 70% sequence identity and can be employed to identify orthologous or paralogous sequences.

20 *D. Polynucleotides Having a Specific Sequence Identity with the Polynucleotides of (A), (B) or (C)*

As indicated in (d), above, the present invention provides isolated nucleic acids comprising polynucleotides of the present invention, wherein the polynucleotides have a specified identity at the nucleotide level to a polynucleotide as disclosed above in paragraphs (A), (B), or (C). The percentage of identity to a reference sequence is at least 60% and, rounded upwards to the nearest integer, can be expressed as an integer selected from the group of integers consisting of from 60 to 99. Thus, for example, the percentage of identity to a reference sequence can be at least 70%, 75%, 80%, 85%, 90%, or 95%.

30 Optionally, the polynucleotides of this embodiment will share an epitope with a polypeptide encoded by the polynucleotides of (A), (B), or (C). Thus, these polynucleotides encode a first polypeptide which elicits production of antisera comprising antibodies which are specifically reactive to a second polypeptide encoded by

a polynucleotide of (A), (B), or (C). However, the first polypeptide does not bind to antisera raised against itself when the antisera has been fully immunosorbed with the first polypeptide. Hence, the polynucleotides of this embodiment can be used to generate antibodies for use in, for example, the screening of expression libraries for nucleic acids comprising polynucleotides of (A), (B), or (C), or for purification of, or in immunoassays for, polypeptides encoded by the polynucleotides of (A), (B), or (C). The polynucleotides of this embodiment embrace nucleic acid sequences which can be employed for selective hybridization to a polynucleotide encoding a polypeptide of the present invention.

Screening polypeptides for specific binding to antisera can be conveniently achieved using peptide display libraries. This method involves the screening of large collections of peptides for individual members having the desired function or structure. Antibody screening of peptide display libraries is well known in the art. The displayed peptide sequences can be from 3 to 5000 or more amino acids in length, frequently from 5-100 amino acids long, and often from about 8 to 15 amino acids long. In addition to direct chemical synthetic methods for generating peptide libraries, several recombinant DNA methods have been described. One type involves the display of a peptide sequence on the surface of a bacteriophage or cell. Each bacteriophage or cell contains the nucleotide sequence encoding the particular displayed peptide sequence. Such methods are described in PCT patent publication Nos. 91/17271, 91/18980, 91/19818, and 93/08278. Other systems for generating libraries of peptides have aspects of both *in vitro* chemical synthesis and recombinant methods. See, PCT Patent publication Nos. 92/05258, 92/14843, and 96/19256. See also, U.S. Patent Nos. 5,658,754; and 5,643,768. Peptide display libraries, vectors, and screening kits are commercially available from such suppliers as Invitrogen (Carlsbad, CA).

E. Polynucleotides Encoding a Protein Having a Subsequence from a Prototype Polypeptide and is Cross-Reactive to the Prototype Polypeptide

As indicated in (e), above, the present invention provides isolated nucleic acids comprising polynucleotides of the present invention, wherein the polynucleotides encode a protein having a subsequence of contiguous amino acids from a prototype polypeptide of the present invention such as are provided in (a), above. The length of contiguous amino acids from the prototype polypeptide is selected from the group of integers

consisting of from at least 10 to the number of amino acids within the prototype sequence. Thus, for example, the polynucleotide can encode a polypeptide having a subsequence having at least 10, 15, 20, 25, 30, 35, 40, 45, or 50, contiguous amino acids from the prototype polypeptide. Further, the number of such subsequences
5 encoded by a polynucleotide of the instant embodiment can be any integer selected from the group consisting of from 1 to 20, such as 2, 3, 4, or 5. The subsequences can be separated by any integer of nucleotides from 1 to the number of nucleotides in the sequence such as at least 5, 10, 15, 25, 50, 100, or 200 nucleotides.

The proteins encoded by polynucleotides of this embodiment, when presented as
10 an immunogen, elicit the production of polyclonal antibodies which specifically bind to a prototype polypeptide such as but not limited to, a polypeptide encoded by the polynucleotide of (a) or (b), above. Generally, however, a protein encoded by a polynucleotide of this embodiment does not bind to antisera raised against the prototype polypeptide when the antisera has been fully immunosorbed with the prototype
15 polypeptide. Methods of making and assaying for antibody binding specificity/affinity are well known in the art. Exemplary immunoassay formats include ELISA, competitive immunoassays, radioimmunoassays, Western blots, indirect immunofluorescent assays and the like.

In a preferred assay method, fully immunosorbed and pooled antisera which is
20 elicited to the prototype polypeptide can be used in a competitive binding assay to test the protein. The concentration of the prototype polypeptide required to inhibit 50% of the binding of the antisera to the prototype polypeptide is determined. If the amount of the protein required to inhibit binding is less than twice the amount of the prototype protein, then the protein is said to specifically bind to the antisera elicited to the
25 immunogen. Accordingly, the proteins of the present invention embrace allelic variants, conservatively modified variants, and minor recombinant modifications to a prototype polypeptide.

A polynucleotide of the present invention optionally encodes a protein having a molecular weight as the non-glycosylated protein within 20% of the molecular weight of
30 the full-length non-glycosylated polypeptides of the present invention. Molecular weight can be readily determined by SDS-PAGE under reducing conditions. Preferably, the molecular weight is within 15% of a full length polypeptide of the present invention, more preferably within 10% or 5%, and most preferably within 3%, 2%, or 1% of a full

length polypeptide of the present invention. Molecular weight determination of a protein can be conveniently performed by SDS-PAGE under denaturing conditions.

Optionally, the polynucleotides of this embodiment will encode a protein having a specific activity at least 50%, 60%, 80%, or 90% of the native, endogenous (i.e., non-isolated), full-length polypeptide of the present invention. Further, the proteins encoded by polynucleotides of this embodiment will optionally have a substantially similar affinity constant (K_m) and/or catalytic activity (i.e., the microscopic rate constant, k_{cat}) as the native endogenous, full-length protein. Those of skill in the art will recognize that k_{cat}/K_m value determines the specificity for competing substrates and is often referred to as the specificity constant. Proteins of this embodiment can have a k_{cat}/K_m value at least 10% of a non-isolated full-length polypeptide of the present invention as determined using the endogenous substrate of that polypeptide. Optionally, the k_{cat}/K_m value will be at least 20%, 30%, 40%, 50%, and most preferably at least 60%, 70%, 80%, 90%, or 95% the k_{cat}/K_m value of the non-isolated, full-length polypeptide of the present invention.

Determination of k_{cat} , K_m , and k_{cat}/K_m can be determined by any number of means well known to those of skill in the art. For example, the initial rates (i.e., the first 5% or less of the reaction) can be determined using rapid mixing and sampling techniques (e.g., continuous-flow, stopped-flow, or rapid quenching techniques), flash photolysis, or relaxation methods (e.g., temperature jumps) in conjunction with such exemplary methods of measuring as spectrophotometry, spectrofluorimetry, nuclear magnetic resonance, or radioactive procedures. Kinetic values are conveniently obtained using a Lineweaver-Burk or Eadie-Hofstee plot.

F. Polynucleotides Complementary to the Polynucleotides of (A)-(E)

As indicated in (f), above, the present invention provides isolated nucleic acids comprising polynucleotides complementary to the polynucleotides of paragraphs A-E, above. As those of skill in the art will recognize, complementary sequences base-pair throughout the entirety of their length with the polynucleotides of (A)-(E) (i.e., have 100% sequence identity over their entire length). Complementary bases associate through hydrogen bonding in double stranded nucleic acids. For example, the following base pairs are complementary: guanine and cytosine; adenine and thymine; and adenine and uracil.

G. Polynucleotides Which are Subsequences of the Polynucleotides of (A)-(F)

As indicated in (g), above, the present invention provides isolated nucleic acids comprising polynucleotides which comprise at least 15 contiguous bases from the polynucleotides of (A) through (F) as discussed above. The length of the polynucleotide
5 is given as an integer selected from the group consisting of from at least 15 to the length of the nucleic acid sequence from which the polynucleotide is a subsequence of. Thus, for example, polynucleotides of the present invention are inclusive of polynucleotides comprising at least 15, 20, 25, 30, 40, 50, 60, 75, or 100 contiguous nucleotides in length from the polynucleotides of (A)-(F). Optionally, the number of such
10 subsequences encoded by a polynucleotide of the instant embodiment can be any integer selected from the group consisting of from 1 to 20, such as 2, 3, 4, or 5. The subsequences can be separated by any integer of nucleotides from 1 to the number of nucleotides in the sequence such as at least 5, 10, 15, 25, 50, 100, or 200 nucleotides.

The subsequences of the present invention can comprise structural characteristics
15 of the sequence from which it is derived. Alternatively, the subsequences can lack certain structural characteristics of the larger sequence from which it is derived. For example, a subsequence from a polynucleotide encoding a polypeptide having at least one linear epitope in common with a prototype polypeptide sequence as provided in (a), above, may encode an epitope in common with the prototype sequence. Alternatively,
20 the subsequence may not encode an epitope in common with the prototype sequence but can be used to isolate the larger sequence by, for example, nucleic acid hybridization with the sequence from which it's derived. Subsequences can be used to modulate or detect gene expression by introducing into the subsequences compounds which bind, intercalate, cleave and/or crosslink to nucleic acids. Exemplary compounds include
25 acridine, psoralen, phenanthroline, naphthoquinone, daunomycin or chloroethylaminoaryl conjugates.

Construction of Nucleic Acids

The isolated nucleic acids of the present invention can be made using (a) standard
30 recombinant methods, (b) synthetic techniques, or combinations thereof. In some embodiments, the polynucleotides of the present invention will be cloned, amplified, or otherwise constructed from a monocot. In preferred embodiments the monocot is *Zea mays*.

The nucleic acids may conveniently comprise sequences in addition to a polynucleotide of the present invention. For example, a multi-cloning site comprising one or more endonuclease restriction sites may be inserted into the nucleic acid to aid in isolation of the polynucleotide. Also, translatable sequences may be inserted to aid in
5 the isolation of the translated polynucleotide of the present invention. For example, a hexa-histidine marker sequence provides a convenient means to purify the proteins of the present invention. A polynucleotide of the present invention can be attached to a vector, adapter, or linker for cloning and/or expression of a polynucleotide of the present invention. Additional sequences may be added to such cloning and/or expression
10 sequences to optimize their function in cloning and/or expression, to aid in isolation of the polynucleotide, or to improve the introduction of the polynucleotide into a cell. Typically, the length of a nucleic acid of the present invention less the length of its polynucleotide of the present invention is less than 20 kilobase pairs, often less than 15 kb, and frequently less than 10 kb. Use of cloning vectors, expression vectors, adapters,
15 and linkers is well known and extensively described in the art. For a description of various nucleic acids see, for example, Stratagene Cloning Systems, Catalogs 1995, 1996, 1997 (La Jolla, CA); and, Amersham Life Sciences, Inc, Catalog '97 (Arlington Heights, IL).

20 *A. Recombinant Methods for Constructing Nucleic Acids*

The isolated nucleic acid compositions of this invention, such as RNA, cDNA, genomic DNA, or a hybrid thereof, can be obtained from plant biological sources using any number of cloning methodologies known to those of skill in the art. In some
25 embodiments, oligonucleotide probes which selectively hybridize, under stringent conditions, to the polynucleotides of the present invention are used to identify the desired sequence in a cDNA or genomic DNA library. While isolation of RNA, and construction of cDNA and genomic libraries is well known to those of ordinary skill in the art, the following highlights some of the methods employed.

30 *A1. mRNA Isolation and Purification*

Total RNA from plant cells comprises such nucleic acids as mitochondrial RNA, chloroplastic RNA, rRNA, tRNA, hnRNA and mRNA. Total RNA preparation typically involves lysis of cells and removal of proteins, followed by precipitation of nucleic

acids. Extraction of total RNA from plant cells can be accomplished by a variety of means. Frequently, extraction buffers include a strong detergent such as SDS and an organic denaturant such as guanidinium isothiocyanate, guanidine hydrochloride or phenol. Following total RNA isolation, poly(A)⁺ mRNA is typically purified from the remainder RNA using oligo(dT) cellulose. Exemplary total RNA and mRNA isolation protocols are described in *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997); and, *Current Protocols in Molecular Biology*, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (1995). Total RNA and mRNA isolation kits are commercially available from vendors such as Stratagene (La Jolla, CA), Clontech (Palo Alto, CA), Pharmacia (Piscataway, NJ), and 5'-3' (Paoli, PA). See also, U.S. Patent Nos. 5,614,391; and, 5,459,253. The mRNA can be fractionated into populations with size ranges of about 0.5, 1.0, 1.5, 2.0, 2.5 or 3.0 kb. The cDNA synthesized for each of these fractions can be size selected to the same size range as its mRNA prior to vector insertion. This method helps eliminate truncated cDNA formed by incompletely reverse transcribed mRNA.

A2. Construction of a cDNA Library

Construction of a cDNA library generally entails five steps. First, first strand cDNA synthesis is initiated from a poly(A)⁺ mRNA template using a poly(dT) primer or random hexanucleotides. Second, the resultant RNA-DNA hybrid is converted into double stranded cDNA, typically by a combination of RNase H and DNA polymerase I (or Klenow fragment). Third, the termini of the double stranded cDNA are ligated to adaptors. Ligation of the adaptors will produce cohesive ends for cloning. Fourth, size selection of the double stranded cDNA eliminates excess adaptors and primer fragments, and eliminates partial cDNA molecules due to degradation of mRNAs or the failure of reverse transcriptase to synthesize complete first strands. Fifth, the cDNAs are ligated into cloning vectors and packaged. cDNA synthesis protocols are well known to the skilled artisan and are described in such standard references as: *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997); and, *Current Protocols in Molecular Biology*, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (1995). cDNA synthesis kits are available from a variety of commercial vendors such as Stratagene or Pharmacia.

A number of cDNA synthesis protocols have been described which provide substantially pure full-length cDNA libraries. Substantially pure full-length cDNA libraries are constructed to comprise at least 90%, and more preferably at least 93% or 95% full-length inserts amongst clones containing inserts. The length of insert in such libraries can be from 0 to 8, 9, 10, 11, 12, 13, or more kilobase pairs. Vectors to accommodate inserts of these sizes are known in the art and available commercially. See, e.g., Stratagene's lambda ZAP Express (cDNA cloning vector with 0 to 12 kb cloning capacity).

An exemplary method of constructing a greater than 95% pure full-length cDNA library is described by Carninci *et al.*, *Genomics*, 37:327-336 (1996). In that protocol, the cap-structure of eukaryotic mRNA is chemically labeled with biotin. By using streptavidin-coated magnetic beads, only the full-length first-strand cDNA/mRNA hybrids are selectively recovered after RNase I treatment. The method provides a high yield library with an unbiased representation of the starting mRNA population. Other methods for producing full-length libraries are known in the art. See, e.g., Edery *et al.*, *Mol. Cell Biol.*, 15(6):3363-3371 (1995); and, PCT Application WO 96/34981.

A3. Normalized or Subtracted cDNA Libraries

A non-normalized cDNA library represents the mRNA population of the tissue it was made from. Since unique clones are out-numbered by clones derived from highly expressed genes their isolation can be laborious. Normalization of a cDNA library is the process of creating a library in which each clone is more equally represented.

A number of approaches to normalize cDNA libraries are known in the art. One approach is based on hybridization to genomic DNA. The frequency of each hybridized cDNA in the resulting normalized library would be proportional to that of each corresponding gene in the genomic DNA. Another approach is based on kinetics. If cDNA reannealing follows second-order kinetics, rarer species anneal less rapidly and the remaining single-stranded fraction of cDNA becomes progressively more normalized during the course of the hybridization. Specific loss of any species of cDNA, regardless of its abundance, does not occur at any Cot value. Construction of normalized libraries is described in Ko, *Nucl. Acids. Res.*, 18(19):5705-5711 (1990); Patanjali *et al.*, *Proc. Natl. Acad. U.S.A.*, 88:1943-1947 (1991); U.S. Patents 5,482,685, and 5,637,685. In an exemplary method described by Soares *et al.*, normalization resulted in reduction of

the abundance of clones from a range of four orders of magnitude to a narrow range of only 1 order of magnitude. *Proc. Natl. Acad. Sci. USA*, 91:9228-9232 (1994).

Subtracted cDNA libraries are another means to increase the proportion of less abundant cDNA species. In this procedure, cDNA prepared from one pool of mRNA is
5 depleted of sequences present in a second pool of mRNA by hybridization. The cDNA:mRNA hybrids are removed and the remaining un-hybridized cDNA pool is enriched for sequences unique to that pool. See, Foote *et al.* in, *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997); Kho and Zarbl, *Technique*, 3(2):58-63 (1991); Sive and St. John, *Nucl. Acids Res.*, 16(22):10937
10 (1988); *Current Protocols in Molecular Biology*, Ausubel, *et al.*, Eds., Greene Publishing and Wiley-Interscience, New York (1995); and, Swaroop *et al.*, *Nucl. Acids Res.*, 19(8):1954 (1991). cDNA subtraction kits are commercially available. See, e.g., PCR-Select (Clontech).

15 A4. Construction of a Genomic Library

To construct genomic libraries, large segments of genomic DNA are generated by random fragmentation, e.g. using restriction endonucleases, and are ligated with vector DNA to form concatemers that can be packaged into the appropriate vector. Methodologies to accomplish these ends, and sequencing methods to verify the sequence
20 of nucleic acids are well known in the art. Examples of appropriate molecular biological techniques and instructions sufficient to direct persons of skill through many construction, cloning, and screening methodologies are found in Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Vols. 1-3 (1989), *Methods in Enzymology*, Vol. 152: *Guide to Molecular Cloning*
25 *Techniques*, Berger and Kimmel, Eds., San Diego: Academic Press, Inc. (1987), *Current Protocols in Molecular Biology*, Ausubel, *et al.*, Eds., Greene Publishing and Wiley-Interscience, New York (1995); *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997). Kits for construction of genomic libraries are also commercially available.

30

A5. Nucleic Acid Screening and Isolation Methods

The cDNA or genomic library can be screened using a probe based upon the sequence of a polynucleotide of the present invention such as those disclosed herein.

Probes may be used to hybridize with genomic DNA or cDNA sequences to isolate homologous genes in the same or different plant species. Those of skill in the art will appreciate that various degrees of stringency of hybridization can be employed in the assay; and either the hybridization or the wash medium can be stringent. As the
5 conditions for hybridization become more stringent, there must be a greater degree of complementarity between the probe and the target for duplex formation to occur. The degree of stringency can be controlled by temperature, ionic strength, pH and the presence of a partially denaturing solvent such as formamide. For example, the stringency of hybridization is conveniently varied by changing the polarity of the reactant
10 solution through manipulation of the concentration of formamide within the range of 0% to 50%. The degree of complementarity (sequence identity) required for detectable binding will vary in accordance with the stringency of the hybridization medium and/or wash medium. The degree of complementarity will optimally be 100 percent; however, it should be understood that minor sequence variations in the probes and primers may be
15 compensated for by reducing the stringency of the hybridization and/or wash medium.

The nucleic acids of interest can also be amplified from nucleic acid samples using amplification techniques. For instance, polymerase chain reaction (PCR) technology can be used to amplify the sequences of polynucleotides of the present invention and related genes directly from genomic DNA or cDNA libraries. PCR and
20 other *in vitro* amplification methods may also be useful, for example, to clone nucleic acid sequences that code for proteins to be expressed, to make nucleic acids to use as probes for detecting the presence of the desired mRNA in samples, for nucleic acid sequencing, or for other purposes. Examples of techniques sufficient to direct persons of skill through *in vitro* amplification methods are found in Berger, Sambrook, and
25 Ausubel, as well as Mullis *et al.*, U.S. Patent No. 4,683,202 (1987); and, *PCR Protocols A Guide to Methods and Applications*, Innis *et al.*, Eds., Academic Press Inc., San Diego, CA (1990). Commercially available kits for genomic PCR amplification are known in the art. See, e.g., Advantage-GC Genomic PCR Kit (Clontech). The T4 gene 32 protein (Boehringer Mannheim) can be used to improve yield of long PCR products.

30 PCR-based screening methods have also been described. Wilfinger *et al.* describe a PCR-based method in which the longest cDNA is identified in the first step so that incomplete clones can be eliminated from study. *BioTechniques*, 22(3): 481-486 (1997). In that method, a primer pair is synthesized with one primer annealing to the 5'

end of the sense strand of the desired cDNA and the other primer to the vector. Clones are pooled to allow large-scale screening. By this procedure, the longest possible clone is identified amongst candidate clones. Further, the PCR product is used solely as a diagnostic for the presence of the desired cDNA and does not utilize the PCR product itself. Such methods are particularly effective in combination with a full-length cDNA construction methodology, above.

B. Synthetic Methods for Constructing Nucleic Acids

The isolated nucleic acids of the present invention can also be prepared by direct chemical synthesis by methods such as the phosphotriester method of Narang *et al.*, *Meth. Enzymol.* 68: 90-99 (1979); the phosphodiester method of Brown *et al.*, *Meth. Enzymol.* 68: 109-151 (1979); the diethylphosphoramidite method of Beaucage *et al.*, *Tetra. Lett.* 22: 1859-1862 (1981); the solid phase phosphoramidite triester method described by Beaucage and Caruthers, *Tetra. Letts.* 22(20): 1859-1862 (1981), *e.g.*, using an automated synthesizer, *e.g.*, as described in Needham-VanDevanter *et al.*, *Nucleic Acids Res.*, 12: 6159-6168 (1984); and, the solid support method of U.S. Patent No. 4,458,066. Chemical synthesis generally produces a single stranded oligonucleotide. This may be converted into double stranded DNA by hybridization with a complementary sequence, or by polymerization with a DNA polymerase using the single strand as a template. One of skill will recognize that while chemical synthesis of DNA is limited to sequences of about 100 bases, longer sequences may be obtained by the ligation of shorter sequences.

Recombinant Expression Cassettes

The present invention further provides recombinant expression cassettes comprising a nucleic acid of the present invention. A nucleic acid sequence coding for the desired polynucleotide of the present invention, for example a cDNA or a genomic sequence encoding a full length polypeptide of the present invention, can be used to construct a recombinant expression cassette which can be introduced into the desired host cell. A recombinant expression cassette will typically comprise a polynucleotide of the present invention operably linked to transcriptional initiation regulatory sequences which will direct the transcription of the polynucleotide in the intended host cell, such as tissues of a transformed plant.

For example, plant expression vectors may include (1) a cloned plant gene under the transcriptional control of 5' and 3' regulatory sequences and (2) a dominant selectable marker. Such plant expression vectors may also contain, if desired, a promoter regulatory region (e.g., one conferring inducible or constitutive, environmentally- or developmentally-regulated, or cell- or tissue-specific/selective expression), a transcription initiation start site, a ribosome binding site, an RNA processing signal, a transcription termination site, and/or a polyadenylation signal.

A plant promoter fragment can be employed which will direct expression of a polynucleotide of the present invention in all tissues of a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'- promoter derived from T-DNA of *Agrobacterium tumefaciens*, the ubiquitin 1 promoter, the Smas promoter, the cinnamyl alcohol dehydrogenase promoter (U.S. Patent No. 5,683,439), the *Nos* promoter, the pEmu promoter, the rubisco promoter, the GRP1-8 promoter, the actin promoter, the F3.7 promoter, and other transcription initiation regions from various plant genes known to those of skill.

Alternatively, the plant promoter can direct expression of a polynucleotide of the present invention in a specific tissue or may be otherwise under more precise environmental or developmental control. Such promoters are referred to here as "inducible" promoters. Environmental conditions that may effect transcription by inducible promoters include pathogen attack, anaerobic conditions, or the presence of light. Examples of inducible promoters are the *Adh1* promoter which is inducible by hypoxia or cold stress, the *Hsp70* promoter which is inducible by heat stress, and the *PPDK* promoter which is inducible by light.

Examples of promoters under developmental control include promoters that initiate transcription only, or preferentially, in certain tissues, such as leaves, roots, fruit, seeds, or flowers. The operation of a promoter may also vary depending on its location in the genome. Thus, an inducible promoter may become fully or partially constitutive in certain locations.

Both heterologous and non-heterologous (i.e., endogenous) promoters can be employed to direct expression of the nucleic acids of the present invention. These

promoters can also be used, for example, in recombinant expression cassettes to drive expression of antisense nucleic acids to reduce, increase, or alter concentration and/or composition of the proteins of the present invention in a desired tissue. Thus, in some embodiments, the nucleic acid construct will comprise a promoter functional in a plant cell, such as in *Zea mays*, operably linked to a polynucleotide of the present invention. Promoters useful in these embodiments include the endogenous promoters driving expression of a polypeptide of the present invention.

In some embodiments, isolated nucleic acids which serve as promoter or enhancer elements can be introduced in the appropriate position (generally upstream) of a non-heterologous form of a polynucleotide of the present invention so as to up or down regulate expression of a polynucleotide of the present invention. For example, endogenous promoters can be altered *in vivo* by mutation, deletion, and/or substitution (see, Kmiec, U.S. Patent 5,565,350; Zarling *et al.*, PCT/US93/03868), or isolated promoters can be introduced into a plant cell in the proper orientation and distance from a gene of the present invention so as to control the expression of the gene. Gene expression can be modulated under conditions suitable for plant growth so as to alter the total concentration and/or alter the composition of the polypeptides of the present invention in plant cell. Thus, the present invention provides compositions, and methods for making, heterologous promoters and/or enhancers operably linked to a native, endogenous (i.e., non-heterologous) form of a polynucleotide of the present invention.

Methods for identifying promoters with a particular expression pattern, in terms of, e.g., tissue type, cell type, stage of development, and/or environmental conditions, are well known in the art. See, e.g., *The Maize Handbook*, Chapters 114-115, Freeling and Walbot, Eds., Springer, New York (1994); *Corn and Corn Improvement*, 3rd edition, Chapter 6, Sprague and Dudley, Eds., American Society of Agronomy, Madison, Wisconsin (1988). A typical step in promoter isolation methods is identification of gene products that are expressed with some degree of specificity in the target tissue. Amongst the range of methodologies are: differential hybridization to cDNA libraries; subtractive hybridization; differential display; differential 2-D protein gel electrophoresis; DNA probe arrays; and isolation of proteins known to be expressed with some specificity in the target tissue. Such methods are well known to those of skill in the art. Commercially available products for identifying promoters are known in the art such as Clontech's (Palo Alto, CA) Universal GenomeWalker Kit.

For the protein-based methods, it is helpful to obtain the amino acid sequence for at least a portion of the identified protein, and then to use the protein sequence as the basis for preparing a nucleic acid that can be used as a probe to identify either genomic DNA directly, or preferably, to identify a cDNA clone from a library prepared from the target tissue. Once such a cDNA clone has been identified, that sequence can be used to identify the sequence at the 5' end of the transcript of the indicated gene. For differential hybridization, subtractive hybridization and differential display, the nucleic acid sequence identified as enriched in the target tissue is used to identify the sequence at the 5' end of the transcript of the indicated gene. Once such sequences are identified, starting either from protein sequences or nucleic acid sequences, any of these sequences identified as being from the gene transcript can be used to screen a genomic library prepared from the target organism. Methods for identifying and confirming the transcriptional start site are well known in the art.

In the process of isolating promoters expressed under particular environmental conditions or stresses, or in specific tissues, or at particular developmental stages, a number of genes are identified that are expressed under the desired circumstances, in the desired tissue, or at the desired stage. Further analysis will reveal expression of each particular gene in one or more other tissues of the plant. One can identify a promoter with activity in the desired tissue or condition but that do not have activity in any other common tissue.

To identify the promoter sequence, the 5' portions of the clones described here are analyzed for sequences characteristic of promoter sequences. For instance, promoter sequence elements include the TATA box consensus sequence (TATAAT), which is usually an AT-rich stretch of 5-10 bp located approximately 20 to 40 base pairs upstream of the transcription start site. Identification of the TATA box is well known in the art. For example, one way to predict the location of this element is to identify the transcription start site using standard RNA-mapping techniques such as primer extension, S1 analysis, and/or RNase protection. To confirm the presence of the AT-rich sequence, a structure-function analysis can be performed involving mutagenesis of the putative region and quantification of the mutation's effect on expression of a linked downstream reporter gene. See, e.g., *The Maize Handbook*, Chapter 114, Freeling and Walbot, Eds., Springer, New York, (1994).

In plants, further upstream from the TATA box, at positions -80 to -100, there is typically a promoter element (i.e., the CAAT box) with a series of adenines surrounding the trinucleotide G (or T) N G. J. Messing *et al.*, in *Genetic Engineering in Plants*, Kosage, Meredith and Hollaender, Eds., pp. 221-227 1983. In maize, there is no well
5 conserved CAAT box but there are several short, conserved protein-binding motifs upstream of the TATA box. These include motifs for the trans-acting transcription factors involved in light regulation, anaerobic induction, hormonal regulation, or anthocyanin biosynthesis, as appropriate for each gene.

Once promoter and/or gene sequences are known, a region of suitable size
10 is selected from the genomic DNA that is 5' to the transcriptional start, or the translational start site, and such sequences are then linked to a coding sequence. If the transcriptional start site is used as the point of fusion, any of a number of possible 5' untranslated regions can be used in between the transcriptional start site and the partial coding sequence. If the translational start site at the 3' end of the specific promoter is
15 used, then it is linked directly to the methionine start codon of a coding sequence.

If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added can be derived from, for
20 example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

An intron sequence can be added to the 5' untranslated region or the coding sequence of the partial coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the
25 transcription unit in both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold. Buchman and Berg, *Mol. Cell Biol.* 8: 4395-4405 (1988); Callis *et al.*, *Genes Dev.* 1: 1183-1200 (1987). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of maize introns Adh1-S intron 1, 2, and
30 6, the Bronze-1 intron are known in the art. See generally, *The Maize Handbook*, Chapter 116, Freeling and Walbot, Eds., Springer, New York (1994).

The vector comprising the sequences from a polynucleotide of the present invention will typically comprise a marker gene which confers a selectable phenotype on

plant cells. Usually, the selectable marker gene will encode antibiotic resistance, with suitable genes including genes coding for resistance to the antibiotic spectinomycin (e.g., the *aada* gene), the streptomycin phosphotransferase (SPT) gene coding for streptomycin resistance, the neomycin phosphotransferase (NPTII) gene encoding kanamycin or geneticin resistance, the hygromycin phosphotransferase (HPT) gene coding for hygromycin resistance, genes coding for resistance to herbicides which act to inhibit the action of acetolactate synthase (ALS), in particular the sulfonylurea-type herbicides (e.g., the acetolactate synthase (ALS) gene containing mutations leading to such resistance in particular the S4 and/or Hra mutations), genes coding for resistance to herbicides which act to inhibit action of glutamine synthase, such as phosphinothricin or basta (e.g., the *bar* gene), or other such genes known in the art. The *bar* gene encodes resistance to the herbicide basta, the *ntpII* gene encodes resistance to the antibiotics kanamycin and geneticin, and the ALS gene encodes resistance to the herbicide chlorsulfuron.

Typical vectors useful for expression of genes in higher plants are well known in the art and include vectors derived from the tumor-inducing (Ti) plasmid of *Agrobacterium tumefaciens* described by Rogers *et al.*, Meth. In Enzymol., 153:253-277 (1987). These vectors are plant integrating vectors in that on transformation, the vectors integrate a portion of vector DNA into the genome of the host plant. Exemplary *A. tumefaciens* vectors useful herein are plasmids pKYLX6 and pKYLX7 of Schardl *et al.*, Gene, 61:1-11 (1987) and Berger *et al.*, Proc. Natl. Acad. Sci. U.S.A., 86:8402-8406 (1989). Another useful vector herein is plasmid pBI101.2 that is available from Clontech Laboratories, Inc. (Palo Alto, CA).

A polynucleotide of the present invention can be expressed in either sense or anti-sense orientation as desired. It will be appreciated that control of gene expression in either sense or anti-sense orientation can have a direct impact on the observable plant characteristics. Antisense technology can be conveniently used to gene expression in plants. To accomplish this, a nucleic acid segment from the desired gene is cloned and operably linked to a promoter such that the anti-sense strand of RNA will be transcribed. The construct is then transformed into plants and the antisense strand of RNA is produced. In plant cells, it has been shown that antisense RNA inhibits gene expression by preventing the accumulation of mRNA which encodes the enzyme of interest, see,

e.g., Sheehy *et al.*, *Proc. Nat'l. Acad. Sci. (USA)* 85: 8805-8809 (1988); and Hiatt *et al.*, U.S. Patent No. 4,801,340.

Another method of suppression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to
5 block the transcription of target genes. For an example of the use of this method to modulate expression of endogenous genes see, Napoli *et al.*, *The Plant Cell* 2: 279-289 (1990) and U.S. Patent No. 5,034,323.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of plant genes. It is possible to design ribozymes that specifically pair with virtually any
10 target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs. The
15 design and use of target RNA-specific ribozymes is described in Haseloff *et al.*, *Nature* 334: 585-591 (1988).

A variety of cross-linking agents, alkylating agents and radical generating species as pendant groups on polynucleotides of the present invention can be used to bind, label, detect, and/or cleave nucleic acids. For example, Vlassov, V. V., *et al.*, *Nucleic Acids
20 Res* (1986) 14:4065-4076, describe covalent bonding of a single-stranded DNA fragment with alkylating derivatives of nucleotides complementary to target sequences. A report of similar work by the same group is that by Knorre, D. G., *et al.*, *Biochimie* (1985) 67:785-789. Iverson and Dervan also showed sequence-specific cleavage of single-stranded DNA mediated by incorporation of a modified nucleotide which was capable of
25 activating cleavage (*J Am Chem Soc* (1987) 109:1241-1243). Meyer, R. B., *et al.*, *J Am Chem Soc* (1989) 111:8517-8519, effect covalent crosslinking to a target nucleotide using an alkylating agent complementary to the single-stranded target nucleotide sequence. A photoactivated crosslinking to single-stranded oligonucleotides mediated by psoralen was disclosed by Lee, B. L., *et al.*, *Biochemistry* (1988) 27:3197-3203. Use of crosslinking
30 in triple-helix forming probes was also disclosed by Home, *et al.*, *J Am Chem Soc* (1990) 112:2435-2437. Use of N⁴, N⁴-ethanocytosine as an alkylating agent to crosslink to single-stranded oligonucleotides has also been described by Webb and Matteucci, *J Am Chem Soc* (1986) 108:2764-2765; *Nucleic Acids Res* (1986) 14:7661-7674; Feteritz

et al., *J. Am. Chem. Soc.* 113:4000 (1991). Various compounds to bind, detect, label, and/or cleave nucleic acids are known in the art. See, for example, U.S. Patent Nos. 5,543,507; 5,672,593; 5,484,908; 5,256,648; and, 5,681,941.

5 **Proteins**

The isolated proteins of the present invention comprise a polypeptide having at least 10 amino acids encoded by any one of the polynucleotides of the present invention as discussed more fully, above, or polypeptides which are conservatively modified variants thereof. The proteins of the present invention or variants thereof can comprise
10 any number of contiguous amino acid residues from a polypeptide of the present invention, wherein that number is selected from the group of integers consisting of from 10 to the number of residues in a full-length polypeptide of the present invention. Optionally, this subsequence of contiguous amino acids is at least 15, 20, 25, 30, 35, or 40 amino acids in length, often at least 50, 60, 70, 80, or 90 amino acids in length.
15 Further, the number of such subsequences can be any integer selected from the group consisting of from 1 to 20, such as 2, 3, 4, or 5.

As those of skill will appreciate, the present invention includes catalytically active polypeptides of the present invention (i.e., enzymes). Catalytically active polypeptides have a specific activity of at least 20%, 30%, or 40%, and preferably at least 50%, 60%,
20 or 70%, and most preferably at least 80%, 90%, or 95% that of the native (non-synthetic), endogenous polypeptide. Further, the substrate specificity (k_{cat}/K_m) is optionally substantially similar to the native (non-synthetic), endogenous polypeptide. Typically, the K_m will be at least 30%, 40%, or 50%, that of the native (non-synthetic), endogenous polypeptide; and more preferably at least 60%, 70%, 80%, or 90%.
25 Methods of assaying and quantifying measures of enzymatic activity and substrate specificity (k_{cat}/K_m), are well known to those of skill in the art.

Generally, the proteins of the present invention will, when presented as an immunogen, elicit production of an antibody specifically reactive to a polypeptide of the present invention. Further, the proteins of the present invention will not bind to antisera
30 raised against a polypeptide of the present invention which has been fully immunosorbed with the same polypeptide. Immunoassays for determining binding are well known to those of skill in the art. A preferred immunoassay is a competitive immunoassay as discussed, *infra*. Thus, the proteins of the present invention can be employed as

immunogens for constructing antibodies immunoreactive to a protein of the present invention for such exemplary utilities as immunoassays or protein purification techniques.

5 **Expression of Proteins in Host Cells**

Using the nucleic acids of the present invention, one may express a protein of the present invention in a recombinantly engineered cell such as bacteria, yeast, insect, mammalian, or preferably plant cells. The cells produce the protein in a non-natural condition (e.g., in quantity, composition, location, and/or time), because they have been
10 genetically altered through human intervention to do so.

It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of a nucleic acid encoding a protein of the present invention. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes will be made.

15 In brief summary, the expression of isolated nucleic acids encoding a protein of the present invention will typically be achieved by operably linking, for example, the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain
20 transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the DNA encoding a protein of the present invention. To obtain high level expression of a cloned gene, it is desirable to construct expression vectors which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation
25 terminator. One of skill would recognize that modifications can be made to a protein of the present invention without diminishing its biological activity. Some modifications may be made to facilitate the cloning, expression, or incorporation of the targeting molecule into a fusion protein. Such modifications are well known to those of skill in the art and include, for example, a methionine added at the amino terminus to provide an
30 initiation site, or additional amino acids (e.g., poly His) placed on either terminus to create conveniently located purification sequences. Restriction sites or termination codons can also be introduced.

A. Expression in Prokaryotes

Prokaryotic cells may be used as hosts for expression. Prokaryotes most frequently are represented by various strains of *E. coli*; however, other microbial strains may also be used. Commonly used prokaryotic control sequences which are defined
5 herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding site sequences, include such commonly used promoters as the beta lactamase (penicillinase) and lactose (lac) promoter systems (Chang et al., Nature 198:1056 (1977)), the tryptophan (trp) promoter system (Goeddel et al., Nucleic
10 Acids Res. 8:4057 (1980)) and the lambda derived P_L promoter and N-gene ribosome binding site (Shimatake et al., Nature 292:128 (1981)). The inclusion of selection markers in DNA vectors transfected in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol.

The vector is selected to allow introduction into the appropriate host cell. Bacterial vectors are typically of plasmid or phage origin. Appropriate bacterial cells are
15 infected with phage vector particles or transfected with naked phage vector DNA. If a plasmid vector is used, the bacterial cells are transfected with the plasmid vector DNA. Expression systems for expressing a protein of the present invention are available using *Bacillus sp.* and *Salmonella* (Palva, et al., Gene 22: 229-235 (1983); Mosbach, et al., Nature 302: 543-545 (1983)).

20

B. Expression in Eukaryotes

A variety of eukaryotic expression systems such as yeast, insect cell lines, plant and mammalian cells, are known to those of skill in the art. As explained briefly below, a of the present invention can be expressed in these eukaryotic systems. In some
25 embodiments, transformed/transfected plant cells, as discussed *infra*, are employed as expression systems for production of the proteins of the instant invention.

Synthesis of heterologous proteins in yeast is well known. Sherman, F., et al., *Methods in Yeast Genetics*, Cold Spring Harbor Laboratory (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Two
30 widely utilized yeast for production of eukaryotic proteins are *Saccharomyces cerevisiae* and *Pichia pastoris*. Vectors, strains, and protocols for expression in *Saccharomyces* and *Pichia* are known in the art and available from commercial suppliers (e.g., Invitrogen). Suitable vectors usually have expression control sequences, such as

promoters, including 3-phosphoglycerate kinase or alcohol oxidase, and an origin of replication, termination sequences and the like as desired.

A protein of the present invention, once expressed, can be isolated from yeast by lysing the cells and applying standard protein isolation techniques to the lysates. The
5 monitoring of the purification process can be accomplished by using Western blot techniques or radioimmunoassay or other standard immunoassay techniques.

The sequences encoding proteins of the present invention can also be ligated to various expression vectors for use in transfecting cell cultures of, for instance, mammalian, insect, or plant origin. Illustrative of cell cultures useful for the production
10 of the peptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines. Expression
15 vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (*e.g.*, the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen *et al.*, *Immunol. Rev.* 89: 49 (1986)), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (*e.g.*, an SV40 large T Ag poly A addition site), and transcriptional terminator sequences. Other animal cells useful for production of
20 proteins of the present invention are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, 1992).

Appropriate vectors for expressing proteins of the present invention in insect cells are usually derived from the SF9 baculovirus. Suitable insect cell lines include mosquito
larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell
25 line (See Schneider, *J. Embryol. Exp. Morphol.* 27: 353-365 (1987)).

As with yeast, when higher animal or plant host cells are employed, polyadenylation or transcription terminator sequences are typically incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also
30 be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, *et al.*, *J. Virol.* 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be incorporated into the vector such as those found in bovine papilloma virus type-vectors. Saveria-Campo, M., Bovine Papilloma Virus DNA a

Eukaryotic Cloning Vector in *DNA Cloning Vol. II a Practical Approach*, D.M. Glover, Ed., IRL Press, Arlington, Virginia pp. 213-238 (1985).

Transfection/Transformation of Cells

5 The method of transformation/transfection is not critical to the instant invention; various methods of transformation or transfection are currently available. As newer methods are available to transform crops or other host cells they may be directly applied. Accordingly, a wide variety of methods have been developed to insert a DNA sequence into the genome of a host cell to obtain the transcription and/or translation of the
10 sequence to effect phenotypic changes in the organism. Thus, any method which provides for efficient transformation/transfection may be employed.

A. Plant Transformation

 A DNA sequence coding for the desired polynucleotide of the present invention,
15 for example a cDNA or a genomic sequence encoding a full length protein, will be used to construct a recombinant expression cassette which can be introduced into the desired plant.

 Isolated nucleic acid acids of the present invention can be introduced into plants according techniques known in the art. Generally, recombinant expression cassettes as
20 described above and suitable for transformation of plant cells are prepared. Techniques for transforming a wide variety of higher plant species are well known and described in the technical, scientific, and patent literature. See, for example, Weising *et al.*, *Ann. Rev. Genet.* 22: 421-477 (1988). For example, the DNA construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation,
25 PEG poration, particle bombardment, silicon fiber delivery, or microinjection of plant cell protoplasts or embryogenic callus. See e.g., Tomes, *et al.*, Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment, pp. 197-213 in *Plant Cell, Tissue and Organ Culture, Fundamental Methods*, (eds. O.L. Gamborg and G.C. Phillips, Springer-Verlag Berlin Heidelberg New York, 1995). Alternatively, the DNA
30 constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent

marker into the plant cell DNA when the cell is infected by the bacteria. See, U.S. Patent No. 5,591,616.

The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski *et al.*, *Embo J.* 3: 2717-2722 (1984). Electroporation
5 techniques are described in Fromm *et al.*, *Proc. Natl. Acad. Sci.* 82: 5824 (1985). Ballistic transformation techniques are described in Klein *et al.*, *Nature* 327: 70-73 (1987).

Agrobacterium tumefaciens-mediated transformation techniques are well described in the scientific literature. See, for example Horsch *et al.*, *Science* 233: 496-498 (1984), and
10 Fraley *et al.*, *Proc. Natl. Acad. Sci.* 80: 4803 (1983). Although *Agrobacterium* is useful primarily in dicots, certain monocots can be transformed by *Agrobacterium*. For instance, *Agrobacterium* transformation of maize is described in U.S. Patent No. 5,550,318.

Other methods of transfection or transformation include (1) *Agrobacterium*
15 *rhizogenes*-mediated transformation (see, e.g., Lichtenstein and Fuller In: Genetic Engineering, vol. 6, PWJ Rigby, Ed., London, Academic Press, 1987; and Lichtenstein, C. P., and Draper, J., In: DNA Cloning, Vol. II, D. M. Glover, Ed., Oxford, IRI Press, 1985), Application PCT/US87/02512 (WO 88/02405 published Apr. 7, 1988) describes the use of *A. rhizogenes* strain A4 and its Ri plasmid along with *A. tumefaciens*
20 vectors pARC8 or pARC16 (2) liposome-mediated DNA uptake (see, e.g., Freeman *et al.*, *Plant Cell Physiol.* 25: 1353, 1984), (3) the vortexing method (see, e.g., Kindle, *Proc. Natl. Acad. Sci.*, USA 87: 1228, (1990).

DNA can also be introduced into plants by direct DNA transfer into pollen as described by Zhou *et al.*, *Methods in Enzymology*, 101:433 (1983); D. Hess, Intern
25 *Rev. Cytol.*, 107:367 (1987); Luo *et al.*, *Plant Mol. Biol. Reporter*, 6:165 (1988). Expression of polypeptide coding genes can be obtained by injection of the DNA into reproductive organs of a plant as described by Pena *et al.*, *Nature*, 325:274 (1987). DNA can also be injected directly into the cells of immature embryos and the rehydration of desiccated embryos as described by Neuhaus *et al.*, *Theor. Appl. Genet.*, 75:30
30 (1987); and Benbrook *et al.*, in *Proceedings Bio Expo 1986*, Butterworth, Stoneham, Mass., pp. 27-54 (1986). A variety of plant viruses that can be employed as vectors are known in the art and include cauliflower mosaic virus (CaMV), geminivirus, brome mosaic virus, and tobacco mosaic virus.

B. Transfection of Prokaryotes, Lower Eukaryotes, and Animal Cells

Animal and lower eukaryotic (e.g., yeast) host cells are competent or rendered competent for transfection by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation, biolistics, and micro-injection of the DNA directly into the cells. The transfected cells are cultured by means well known in the art. Kuchler, R.J., *Biochemical Methods in Cell Culture and Virology*, Dowden, Hutchinson and Ross, Inc. (1977).

Synthesis of Proteins

The proteins of the present invention can be constructed using non-cellular synthetic methods. Solid phase synthesis of proteins of less than about 50 amino acids in length may be accomplished by attaching the C-terminal amino acid of the sequence to an insoluble support followed by sequential addition of the remaining amino acids in the sequence. Techniques for solid phase synthesis are described by Barany and Merrifield, *Solid-Phase Peptide Synthesis*, pp. 3-284 in *The Peptides: Analysis, Synthesis, Biology. Vol. 2: Special Methods in Peptide Synthesis, Part A.*; Merrifield, et al., *J. Am. Chem. Soc.* 85: 2149-2156 (1963), and Stewart et al., *Solid Phase Peptide Synthesis, 2nd ed.*, Pierce Chem. Co., Rockford, Ill. (1984). Proteins of greater length may be synthesized by condensation of the amino and carboxy termini of shorter fragments. Methods of forming peptide bonds by activation of a carboxy terminal end (e.g., by the use of the coupling reagent N,N'-dicyclohexylcarbodiimide) is known to those of skill.

Purification of Proteins

The proteins of the present invention may be purified by standard techniques well known to those of skill in the art. Recombinantly produced proteins of the present invention can be directly expressed or expressed as a fusion protein. The recombinant protein is purified by a combination of cell lysis (e.g., sonication, French press) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired recombinant protein.

The proteins of this invention, recombinant or synthetic, may be purified to substantial purity by standard techniques well known in the art, including detergent

solubilization, selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag: New York (1982); Deutscher, *Guide to Protein Purification*, Academic Press (1990). For example,
5 antibodies may be raised to the proteins as described herein. Purification from *E. coli* can be achieved following procedures described in U.S. Patent No. 4,511,503. The protein may then be isolated from cells expressing the protein and further purified by standard protein chemistry techniques as described herein. Detection of the expressed protein is achieved by methods known in the art and include, for example,
10 radioimmunoassays, Western blotting techniques or immunoprecipitation.

Transgenic Plant Regeneration

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed
15 genotype. Such regeneration techniques often rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker which has been introduced together with a polynucleotide of the present invention. For transformation and regeneration of maize see, Gordon-Kamm *et al.*, *The Plant Cell*, 2:603-618 (1990).

20 Plants cells transformed with a plant expression vector can be regenerated, e.g., from single cells, callus tissue or leaf discs according to standard plant tissue culture techniques. It is well known in the art that various cells, tissues, and organs from almost any plant can be successfully cultured to regenerate an entire plant. Plant regeneration from cultured protoplasts is described in Evans *et al.*, *Protoplasts Isolation and Culture*,
25 *Handbook of Plant Cell Culture*, Macmillilan Publishing Company, New York, pp. 124-176 (1983); and Binding, *Regeneration of Plants, Plant Protoplasts*, CRC Press, Boca Raton, pp. 21-73 (1985).

The regeneration of plants containing the foreign gene introduced by *Agrobacterium* from leaf explants can be achieved as described by Horsch *et al.*,
30 *Science*, 227:1229-1231 (1985). In this procedure, transformants are grown in the presence of a selection agent and in a medium that induces the regeneration of shoots in the plant species being transformed as described by Fraley *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, 80:4803 (1983). This procedure typically produces shoots within two to four

weeks and these transformant shoots are then transferred to an appropriate root-inducing medium containing the selective agent and an antibiotic to prevent bacterial growth.

Transgenic plants of the present invention may be fertile or sterile.

5 Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee *et al.*, *Ann. Rev. of Plant Phys.* 38: 467-486 (1987). The regeneration of plants from either single plant protoplasts or various explants is well known in the art. See, for example, *Methods for Plant Molecular Biology*, A. Weissbach and H. Weissbach, eds., Academic Press, Inc., San Diego, Calif. (1988). This regeneration and growth process includes the steps of
10 selection of transformant cells and shoots, rooting the transformant shoots and growth of the plantlets in soil. For maize cell culture and regeneration see generally, *The Maize Handbook*, Freeling and Walbot, Eds., Springer, New York (1994); *Corn and Corn Improvement*, 3rd edition, Sprague and Dudley Eds., American Society of Agronomy, Madison, Wisconsin (1988).

15 One of skill will recognize that after the recombinant expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

 In vegetatively propagated crops, mature transgenic plants can be propagated by
20 the taking of cuttings or by tissue culture techniques to produce multiple identical plants. Selection of desirable transgenics is made and new varieties are obtained and propagated vegetatively for commercial use. In seed propagated crops, mature transgenic plants can be self crossed to produce a homozygous inbred plant. The inbred plant produces seed containing the newly introduced heterologous nucleic acid. These seeds can be
25 grown to produce plants that would produce the selected phenotype.

 Parts obtained from the regenerated plant, such as flowers, seeds, leaves, branches, fruit, and the like are included in the invention, provided that these parts comprise cells comprising the isolated nucleic acid of the present invention. Progeny and variants, and mutants of the regenerated plants are also included within the scope of the
30 invention, provided that these parts comprise the introduced nucleic acid sequences.

 Transgenic plants expressing the selectable marker can be screened for transmission of the nucleic acid of the present invention by, for example, standard immunoblot and DNA detection techniques. Transgenic lines are also typically evaluated

on levels of expression of the heterologous nucleic acid. Expression at the RNA level can be determined initially to identify and quantitate expression-positive plants. Standard techniques for RNA analysis can be employed and include PCR amplification assays using oligonucleotide primers designed to amplify only the heterologous RNA templates and solution hybridization assays using heterologous nucleic acid-specific probes. The RNA-positive plants can then analyzed for protein expression by Western immunoblot analysis using the specifically reactive antibodies of the present invention. In addition, *in situ* hybridization and immunocytochemistry according to standard protocols can be done using heterologous nucleic acid specific polynucleotide probes and antibodies, respectively, to localize sites of expression within transgenic tissue. Generally, a number of transgenic lines are usually screened for the incorporated nucleic acid to identify and select plants with the most appropriate expression profiles.

A preferred embodiment is a transgenic plant that is homozygous for the added heterologous nucleic acid; i.e., a transgenic plant that contains two added nucleic acid sequences, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) a heterozygous transgenic plant that contains a single added heterologous nucleic acid, germinating some of the seed produced and analyzing the resulting plants produced for altered expression of a polynucleotide of the present invention relative to a control plant (i.e., native, non-transgenic). Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated.

Modulating Polypeptide Levels and/or Composition

The present invention further provides a method for modulating (i.e., increasing or decreasing) the concentration or composition of the polypeptides of the present invention in a plant or part thereof. Modulation can be effected by increasing or decreasing the concentration and/or the composition (i.e., the ratio of the polypeptides of the present invention) in a plant. The method comprises transforming a plant cell with a recombinant expression cassette comprising a polynucleotide of the present invention as described above to obtain a transformed plant cell, growing the transformed plant cell under plant forming conditions, and inducing expression of a polynucleotide of the present invention in the plant for a time sufficient to modulate concentration and/or composition in the plant or plant part.

In some embodiments, the content and/or composition of polypeptides of the present invention in a plant may be modulated by altering, *in vivo* or *in vitro*, the promoter of a non-isolated gene of the present invention to up- or down-regulate gene expression. In some embodiments, the coding regions of native genes of the present invention can be altered via substitution, addition, insertion, or deletion to decrease activity of the encoded enzyme. See, e.g., Kmiec, U.S. Patent 5,565,350; Zarling *et al.*, PCT/US93/03868. And in some embodiments, an isolated nucleic acid (e.g., a vector) comprising a promoter sequence is transfected into a plant cell. Subsequently, a plant cell comprising the promoter operably linked to a polynucleotide of the present invention is selected for by means known to those of skill in the art such as, but not limited to, Southern blot, DNA sequencing, or PCR analysis using primers specific to the promoter and to the gene and detecting amplicons produced therefrom. A plant or plant part altered or modified by the foregoing embodiments is grown under plant forming conditions for a time sufficient to modulate the concentration and/or composition of polypeptides of the present invention in the plant. Plant forming conditions are well known in the art and discussed briefly, *above*.

In general, concentration or composition is increased or decreased by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% relative to a native control plant, plant part, or cell lacking the aforementioned recombinant expression cassette. Modulation in the present invention may occur during and/or subsequent to growth of the plant to the desired stage of development. Modulating nucleic acid expression temporally and/or in particular tissues can be controlled by employing the appropriate promoter operably linked to a polynucleotide of the present invention in, for example, sense or antisense orientation as discussed in greater detail, *above*. Induction of expression of a polynucleotide of the present invention can also be controlled by exogenous administration of an effective amount of inducing compound. Inducible promoters and inducing compounds which activate expression from these promoters are well known in the art. In preferred embodiments, the polypeptides of the present invention are modulated in monocots, particularly maize.

30

Molecular Markers

The present invention provides a method of genotyping a plant comprising a polynucleotide of the present invention. Preferably, the plant is a monocot, such as maize or sorghum. Genotyping provides a means of distinguishing homologs of a chromosome pair and can be used to differentiate segregants in a plant population.

5 Molecular marker methods can be used for phylogenetic studies, characterizing genetic relationships among crop varieties, identifying crosses or somatic hybrids, localizing chromosomal segments affecting monogenic traits, map based cloning, and the study of quantitative inheritance. See, e.g., *Plant Molecular Biology: A Laboratory Manual*, Chapter 7, Clark, Ed., Springer-Verlag, Berlin (1997). For molecular marker methods,
10 see generally, *The DNA Revolution* by Andrew H. Paterson 1996 (Chapter 2) in: *Genome Mapping in Plants* (ed. Andrew H. Paterson) by Academic Press/R. G. Landis Company, Austin, Texas, pp.7-21.

The particular method of genotyping in the present invention may employ any number of molecular marker analytic techniques such as, but not limited to, restriction
15 fragment length polymorphisms (RFLPs). RFLPs are the product of allelic differences between DNA restriction fragments caused by nucleotide sequence variability. As is well known to those of skill in the art, RFLPs are typically detected by extraction of genomic DNA and digestion with a restriction enzyme. Generally, the resulting fragments are separated according to size and hybridized with a probe; single copy
20 probes are preferred. Restriction fragments from homologous chromosomes are revealed. Differences in fragment size among alleles represent an RFLP. Thus, the present invention further provides a means to follow segregation of a gene or nucleic acid of the present invention as well as chromosomal sequences genetically linked to these genes or nucleic acids using such techniques as RFLP analysis. Linked
25 chromosomal sequences are within 50 centiMorgans (cM), often within 40 or 30 cM, preferably within 20 or 10 cM, more preferably within 5, 3, 2, or 1 cM of a gene of the present invention.

In the present invention, the nucleic acid probes employed for molecular marker mapping of plant nuclear genomes selectively hybridize, under selective hybridization
30 conditions, to a gene encoding a polynucleotide of the present invention. In preferred embodiments, the probes are selected from polynucleotides of the present invention. Typically, these probes are cDNA probes or *Pst* I genomic clones. The length of the probes is discussed in greater detail, above, but are typically at least 15 bases in length,

more preferably at least 20, 25, 30, 35, 40, or 50 bases in length. Generally, however, the probes are less than about 1 kilobase in length. Preferably, the probes are single copy probes that hybridize to a unique locus in a haploid chromosome complement. Some exemplary restriction enzymes employed in RFLP mapping are *EcoRI*, *EcoRV*, and *SsrI*. As used herein the term "restriction enzyme" includes reference to a composition that recognizes and, alone or in conjunction with another composition, cleaves at a specific nucleotide sequence.

The method of detecting an RFLP comprises the steps of (a) digesting genomic DNA of a plant with a restriction enzyme; (b) hybridizing a nucleic acid probe, under selective hybridization conditions, to a sequence of a polynucleotide of the present of said genomic DNA; (c) detecting therefrom a RFLP. Other methods of differentiating polymorphic (allelic) variants of polynucleotides of the present invention can be had by utilizing molecular marker techniques well known to those of skill in the art including such techniques as: 1) single stranded conformation analysis (SSCP); 2) denaturing gradient gel electrophoresis (DGGE); 3) RNase protection assays; 4) allele-specific oligonucleotides (ASOs); 5) the use of proteins which recognize nucleotide mismatches, such as the *E. coli* mutS protein; and 6) allele-specific PCR. Other approaches based on the detection of mismatches between the two complementary DNA strands include clamped denaturing gel electrophoresis (CDGE); heteroduplex analysis (HA); and chemical mismatch cleavage (CMC). Exemplary polymorphic variants are provided in Table I, above. Thus, the present invention further provides a method of genotyping comprising the steps of contacting, under stringent hybridization conditions, a sample suspected of comprising a polynucleotide of the present invention with a nucleic acid probe. Generally, the sample is a plant sample; preferably, a sample suspected of comprising a maize polynucleotide of the present invention (e.g., gene, mRNA). The nucleic acid probe selectively hybridizes, under stringent conditions, to a subsequence of a polynucleotide of the present invention comprising a polymorphic marker. Selective hybridization of the nucleic acid probe to the polymorphic marker nucleic acid sequence yields a hybridization complex. Detection of the hybridization complex indicates the presence of that polymorphic marker in the sample. In preferred embodiments, the nucleic acid probe comprises a polynucleotide of the present invention.

UTR's and Codon Preference

In general, translational efficiency has been found to be regulated by specific sequence elements in the 5' non-coding or untranslated region (5' UTR) of the RNA. Positive sequence motifs include translational initiation consensus sequences (Kozak, *Nucleic Acids Res.* 15:8125 (1987)) and the 7-methylguanosine cap structure (Drummond *et al.*, *Nucleic Acids Res.* 13:7375 (1985)). Negative elements include stable intramolecular 5' UTR stem-loop structures (Muesing *et al.*, *Cell* 48:691 (1987)) and AUG sequences or short open reading frames preceded by an appropriate AUG in the 5' UTR (Kozak, above, Rao *et al.*, *Mol. and Cell. Biol.* 8:284 (1988)). Accordingly, the present invention provides 5' and/or 3' UTR regions for modulation of translation of heterologous coding sequences.

Further, the polypeptide-encoding segments of the polynucleotides of the present invention can be modified to alter codon usage. Altered codon usage can be employed to alter translational efficiency and/or to optimize the coding sequence for expression in a desired host or to optimize the codon usage in a heterologous sequence for expression in maize. Codon usage in the coding regions of the polynucleotides of the present invention can be analyzed statistically using commercially available software packages such as "Codon Preference" available from the University of Wisconsin Genetics Computer Group (see Devereaux *et al.*, *Nucleic Acids Res.* 12: 387-395 (1984)) or MacVector 4.1 (Eastman Kodak Co., New Haven, Conn.). Thus, the present invention provides a codon usage frequency characteristic of the coding region of at least one of the polynucleotides of the present invention. The number of polynucleotides that can be used to determine a codon usage frequency can be any integer from 1 to the number of polynucleotides of the present invention as provided herein. Optionally, the polynucleotides will be full-length sequences. An exemplary number of sequences for statistical analysis can be at least 1, 5, 10, 20, 50, or 100.

Sequence Shuffling

The present invention provides methods for sequence shuffling using polynucleotides of the present invention, and compositions resulting therefrom. Sequence shuffling is described in PCT publication No. 96/19256. See also, Zhang, J.-H., *et al. Proc. Natl. Acad. Sci. USA* 94:4504-4509 (1997). Generally, sequence shuffling provides a means for generating libraries of polynucleotides having a desired characteristic which can be selected or screened for. Libraries of recombinant

polynucleotides are generated from a population of related sequence polynucleotides which comprise sequence regions which have substantial sequence identity and can be homologously recombined in vitro or in vivo. The population of sequence-recombined polynucleotides comprises a subpopulation of polynucleotides which possess desired or advantageous characteristics and which can be selected by a suitable selection or screening method. The characteristics can be any property or attribute capable of being selected for or detected in a screening system, and may include properties of: an encoded protein, a transcriptional element, a sequence controlling transcription, RNA processing, RNA stability, chromatin conformation, translation, or other expression property of a gene or transgene, a replicative element, a protein-binding element, or the like, such as any feature which confers a selectable or detectable property. In some embodiments, the selected characteristic will be a decreased K_m and/or increased K_{cat} over the wild-type protein as provided herein. In other embodiments, a protein or polynucleotide generated from sequence shuffling will have a ligand binding affinity greater than the non-shuffled wild-type polynucleotide. The increase in such properties can be at least 110%, 120%, 130%, 140% or at least 150% of the wild-type value.

Generic and Consensus Sequences

Polynucleotides and polypeptides of the present invention further include those having: (a) a generic sequence of at least two homologous polynucleotides or polypeptides, respectively, of the present invention; and, (b) a consensus sequence of at least three homologous polynucleotides or polypeptides, respectively, of the present invention. The generic sequence of the present invention comprises each species of polypeptide or polynucleotide embraced by the generic polypeptide or polynucleotide, sequence, respectively. The individual species encompassed by a polynucleotide having an amino acid or nucleic acid consensus sequence can be used to generate antibodies or produce nucleic acid probes or primers to screen for homologs in other species, genera, families, orders, classes, phyla, or kingdoms. For example, a polynucleotide having a consensus sequences from a gene family of *Zea mays* can be used to generate antibody or nucleic acid probes or primers to other *Gramineae* species such as wheat, rice, or sorghum. Alternatively, a polynucleotide having a consensus sequence generated from orthologous genes can be used to identify or isolate orthologs of other taxa. Typically, a polynucleotide having a consensus sequence will be at least 9, 10, 15, 20, 25, 30, or 40

amino acids in length, or 20, 30, 40, 50, 100, or 150 nucleotides in length. As those of skill in the art are aware, a conservative amino acid substitution can be used for amino acids which differ amongst aligned sequence but are from the same conservative substitution group as discussed above. Optionally, no more than 1 or 2 conservative amino acids are substituted for each 10 amino acid length of consensus sequence.

Similar sequences used for generation of a consensus or generic sequence include any number and combination of allelic variants of the same gene, orthologous, or paralogous sequences as provided herein. Optionally, similar sequences used in generating a consensus or generic sequence are identified using the BLAST algorithm's smallest sum probability (P(N)). Various suppliers of sequence-analysis software are listed in chapter 7 of *Current Protocols in Molecular Biology*, F.M. Ausubel *et al.*, Eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (Supplement 30). A polynucleotide sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, or 0.001, and most preferably less than about 0.0001, or 0.00001. Similar polynucleotides can be aligned and a consensus or generic sequence generated using multiple sequence alignment software available from a number of commercial suppliers such as the Genetics Computer Group's (Madison, WI) PILEUP software, Vector NTI's (North Bethesda, MD) ALIGNX, or Genecode's (Ann Arbor, MI) SEQUENCHER. Conveniently, default parameters of such software can be used to generate consensus or generic sequences.

Detection of Nucleic Acids

The present invention further provides methods for detecting a polynucleotide of the present invention in a nucleic acid sample suspected of comprising a polynucleotide of the present invention, such as a plant cell lysate, particularly a lysate of corn. In some embodiments, a gene of the present invention or portion thereof can be amplified prior to the step of contacting the nucleic acid sample with a polynucleotide of the present invention. The nucleic acid sample is contacted with the polynucleotide to form a hybridization complex. The polynucleotide hybridizes under stringent conditions to a gene encoding a polypeptide of the present invention. Formation of the hybridization complex is used to detect a gene encoding a polypeptide of the present invention in the

nucleic acid sample. Those of skill will appreciate that an isolated nucleic acid comprising a polynucleotide of the present invention should lack cross-hybridizing sequences in common with non-target genes that would yield a false positive result.

Detection of the hybridization complex can be achieved using any number of well known methods. For example, the nucleic acid sample, or a portion thereof, may be assayed by hybridization formats including but not limited to, solution phase, solid phase, mixed phase, or *in situ* hybridization assays. Briefly, in solution (or liquid) phase hybridizations, both the target nucleic acid and the probe or primer are free to interact in the reaction mixture. In solid phase hybridization assays, probes or primers are typically linked to a solid support where they are available for hybridization with target nucleic in solution. In mixed phase, nucleic acid intermediates in solution hybridize to target nucleic acids in solution as well as to a nucleic acid linked to a solid support. In *in situ* hybridization, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybridization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the various hybridization assay formats: Singer *et al.*, *Biotechniques* 4(3): 230-250 (1986); Haase *et al.*, *Methods in Virology*, Vol. VII, pp. 189-226 (1984); Wilkinson, The theory and practice of *in situ* hybridization in: *In situ Hybridization*, D.G. Wilkinson, Ed., IRL Press, Oxford University Press, Oxford; and *Nucleic Acid Hybridization: A Practical Approach*, Hames, B.D. and Higgins, S.J., Eds., IRL Press (1987).

Nucleic Acid Labels and Detection Methods

The means by which nucleic acids of the present invention are labeled is not a critical aspect of the present invention and can be accomplished by any number of methods currently known or later developed. Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, radioisotopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads, fluorescent dyes (*e.g.*, fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (*e.g.*, ^3H , ^{125}I , ^{35}S , ^{14}C , or ^{32}P), enzymes (*e.g.*, horse radish peroxidase, alkaline phosphatase and others commonly used

in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (*e.g.*, polystyrene, polypropylene, latex, etc.) beads.

Nucleic acids of the present invention can be labeled by any one of several methods typically used to detect the presence of hybridized nucleic acids. One common method of detection is the use of autoradiography using probes labeled with ^3H , ^{125}I , ^{35}S , ^{14}C , or ^{32}P , or the like. The choice of radio-active isotope depends on research preferences due to ease of synthesis, stability, and half lives of the selected isotopes. Other labels include ligands which bind to antibodies labeled with fluorophores, chemiluminescent agents, and enzymes. Alternatively, probes can be conjugated directly with labels such as fluorophores, chemiluminescent agents or enzymes. The choice of label depends on sensitivity required, ease of conjugation with the probe, stability requirements, and available instrumentation. Labeling the nucleic acids of the present invention is readily achieved such as by the use of labeled PCR primers.

In some embodiments, the label is simultaneously incorporated during the amplification step in the preparation of the nucleic acids. Thus, for example, polymerase chain reaction (PCR) with labeled primers or labeled nucleotides will provide a labeled amplification product. In another embodiment, transcription amplification using a labeled nucleotide (*e.g.*, fluorescein-labeled UTP and/or CTP) incorporates a label into the transcribed nucleic acids.

Non-radioactive probes are often labeled by indirect means. For example, a ligand molecule is covalently bound to the probe. The ligand then binds to an anti-ligand molecule which is either inherently detectable or covalently bound to a detectable signal system, such as an enzyme, a fluorophore, or a chemiluminescent compound. Enzymes of interest as labels will primarily be hydrolases, such as phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc. Chemiluminescers include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. Ligands and anti-ligands may be varied widely. Where a ligand has a natural anti-ligand, namely ligands such as biotin, thyroxine, and cortisol, it can be used in conjunction with its labeled, naturally occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an antibody.

Probes can also be labeled by direct conjugation with a label. For example, cloned DNA probes have been coupled directly to horseradish peroxidase or alkaline phosphatase, (Renz, M., and Kurz, K., *A Colorimetric Method for DNA Hybridization*, *Nucl. Acids Res.* 12: 3435-3444 (1984)) and synthetic oligonucleotides have been
5 coupled directly with alkaline phosphatase (Jablonski, E., *et al.*, *Preparation of Oligodeoxynucleotide-Alkaline Phosphatase Conjugates and Their Use as Hybridization Probes*, *Nuc. Acids. Res.* 14: 6115-6128 (1986); and Li P., *et al.*, *Enzyme-linked Synthetic Oligonucleotide probes: Non-Radioactive Detection of Enterotoxigenic Escherichia Coli in Faeca Specimens*, *Nucl. Acids Res.* 15: 5275-5287 (1987)).
10 Means of detecting such labels are well known to those of skill in the art. Thus, for example, radiolabels may be detected using photographic film or scintillation counters, fluorescent markers may be detected using a photodetector to detect emitted light. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting the reaction product produced by the action of the enzyme on the substrate,
15 and colorimetric labels are detected by simply visualizing the colored label.

Antibodies to Proteins

Antibodies can be raised to a protein of the present invention, including individual, allelic, strain, or species variants, and fragments thereof, both in their
20 naturally occurring (full-length) forms and in recombinant forms. Additionally, antibodies are raised to these proteins in either their native configurations or in non-native configurations. Anti-idiotypic antibodies can also be generated. Many methods of making antibodies are known to persons of skill. The following discussion is presented as a general overview of the techniques available; however, one of skill will
25 recognize that many variations upon the following methods are known.

A number of immunogens are used to produce antibodies specifically reactive with a protein of the present invention. An isolated recombinant, synthetic, or native polynucleotide of the present invention are the preferred immunogens (antigen) for the production of monoclonal or polyclonal antibodies. Those of skill will readily
30 understand that the proteins of the present invention are typically denatured, and optionally reduced, prior to formation of antibodies for screening expression libraries or other assays in which a putative protein of the present invention is expressed or

denatured in a non-native secondary, tertiary, or quaternary structure. Non-isolated polypeptides of the present invention can be used either in pure or impure form.

The protein of the present invention is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies can be generated for
5 subsequent use in immunoassays to measure the presence and quantity of the protein of the present invention. Methods of producing polyclonal antibodies are known to those of skill in the art. In brief, an immunogen (antigen), preferably a purified protein, a protein coupled to an appropriate carrier (*e.g.*, GST, keyhole limpet hemocyanin, *etc.*), or a protein incorporated into an immunization vector such as a recombinant vaccinia virus
10 (*see*, U.S. Patent No. 4,722,848) is mixed with an adjuvant and animals are immunized with the mixture. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the protein of interest. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the
15 antisera to enrich for antibodies reactive to the protein is performed where desired (*See, e.g.*, Coligan, *Current Protocols in Immunology*, Wiley/Greene, NY (1991); and Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press, NY (1989)).

Antibodies, including binding fragments and single chain recombinant versions thereof, against predetermined fragments of a protein of the present invention are raised
20 by immunizing animals, *e.g.*, with conjugates of the fragments with carrier proteins as described above. Typically, the immunogen of interest is a protein of at least about 5 amino acids, more typically the protein is 10 amino acids in length, preferably, 15 amino acids in length and more preferably the protein is 20 amino acids in length or greater. The peptides are typically coupled to a carrier protein (*e.g.*, as a fusion protein), or are
25 recombinantly expressed in an immunization vector. Antigenic determinants on peptides to which antibodies bind are typically 3 to 10 amino acids in length.

Monoclonal antibodies are prepared from cells secreting the desired antibody. Monoclonal antibodies are screened for binding to a protein from which the immunogen was derived. Specific monoclonal and polyclonal antibodies will usually have an
30 antibody binding site with an affinity constant for its cognate monovalent antigen at least between 10^6 - 10^7 , usually at least 10^8 , preferably at least 10^9 , more preferably at least 10^{10} , and most preferably at least 10^{11} liters/mole.

In some instances, it is desirable to prepare monoclonal antibodies from various mammalian hosts, such as mice, rodents, primates, humans, *etc.* Description of techniques for preparing such monoclonal antibodies are found in, *e.g.*, *Basic and Clinical Immunology*, 4th ed., Stites *et al.*, Eds., Lange Medical Publications, Los Altos, CA, and references cited therein; Harlow and Lane, *Supra*; Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd ed., Academic Press, New York, NY (1986); and Kohler and Milstein, *Nature* 256: 495-497 (1975). Summarized briefly, this method proceeds by injecting an animal with an immunogen comprising a protein of the present invention. The animal is then sacrificed and cells taken from its spleen, which are fused with myeloma cells. The result is a hybrid cell or "hybridoma" that is capable of reproducing *in vitro*. The population of hybridomas is then screened to isolate individual clones, each of which secrete a single antibody species to the immunogen. In this manner, the individual antibody species obtained are the products of immortalized and cloned single B cells from the immune animal generated in response to a specific site recognized on the immunogenic substance.

Other suitable techniques involve selection of libraries of recombinant antibodies in phage or similar vectors (*see, e.g.*, Huse *et al.*, *Science* 246: 1275-1281 (1989); and Ward, *et al.*, *Nature* 341: 544-546 (1989); and Vaughan *et al.*, *Nature Biotechnology*, 14: 309-314 (1996)). Alternatively, high avidity human monoclonal antibodies can be obtained from transgenic mice comprising fragments of the unrearranged human heavy and light chain Ig loci (*i.e.*, minilocus transgenic mice). Fishwild *et al.*, *Nature Biotech.*, 14: 845-851 (1996). Also, recombinant immunoglobulins may be produced. See, Cabilly, U.S. Patent No. 4,816,567; and Queen *et al.*, *Proc. Nat'l Acad. Sci.* 86: 10029-10033 (1989).

The antibodies of this invention are also used for affinity chromatography in isolating proteins of the present invention. Columns are prepared, *e.g.*, with the antibodies linked to a solid support, *e.g.*, particles, such as agarose, Sephadex, or the like, where a cell lysate is passed through the column, washed, and treated with increasing concentrations of a mild denaturant, whereby purified protein are released.

The antibodies can be used to screen expression libraries for particular expression products such as normal or abnormal protein. Usually the antibodies in such a procedure are labeled with a moiety allowing easy detection of presence of antigen by antibody binding.

Antibodies raised against a protein of the present invention can also be used to raise anti-idiotypic antibodies. These are useful for detecting or diagnosing various pathological conditions related to the presence of the respective antigens.

5 Frequently, the proteins and antibodies of the present invention will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionucleotides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, chemiluminescent moieties, magnetic particles, and the like.

10

Protein Immunoassays

Means of detecting the proteins of the present invention are not critical aspects of the present invention. In a preferred embodiment, the proteins are detected and/or quantified using any of a number of well recognized immunological binding assays (see, 15 e.g., U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, see also *Methods in Cell Biology*, Vol. 37: *Antibodies in Cell Biology*, Asai, Ed., Academic Press, Inc. New York (1993); *Basic and Clinical Immunology* 7th Edition, Stites & Terr, Eds. (1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, e.g., those 20 reviewed in *Enzyme Immunoassay*, Maggio, Ed., CRC Press, Boca Raton, Florida (1980); Tijan, *Practice and Theory of Enzyme Immunoassays, Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers B.V., Amsterdam (1985); Harlow and Lane, above; *Immunoassay: A Practical Guide*, Chan, Ed., Academic Press, Orlando, FL (1987); *Principles and Practice of Immunoassays*, Price and Newman Eds., Stockton Press, NY (1991); and *Non-isotopic Immunoassays*, Ngo, 25 Ed., Plenum Press, NY (1988). Immunological binding assays (or immunoassays) typically utilize a "capture agent" to specifically bind to and often immobilize the analyte (in this case, a protein of the present invention). The capture agent is a moiety that specifically binds to the analyte. In a preferred embodiment, the capture agent is an 30 antibody that specifically binds a protein(s) of the present invention. The antibody may be produced by any of a number of means known to those of skill in the art as described herein.

Immunoassays also often utilize a labeling agent to specifically bind to and label the binding complex formed by the capture agent and the analyte. The labeling agent may itself be one of the moieties comprising the antibody/analyte complex. Thus, the labeling agent may be a labeled protein of the present invention or a labeled antibody specifically reactive to a protein of the present invention. Alternatively, the labeling agent may be a third moiety, such as another antibody, that specifically binds to the antibody/protein complex.

In a preferred embodiment, the labeling agent is a second antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second can be modified with a detectable moiety, such as biotin, to which a third labeled molecule can specifically bind, such as enzyme-labeled streptavidin.

Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins are normal constituents of the cell walls of streptococcal bacteria. They exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (See, generally Kronval, *et al.*, *J. Immunol.* 111: 1401-1406 (1973), and Akerstrom, *et al.*, *J. Immunol.* 135: 2589-2542 (1985)).

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, preferably from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, analyte, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

While the details of the immunoassays of the present invention may vary with the particular format employed, the method of detecting a protein of the present invention in a biological sample generally comprises the steps of contacting the biological sample with an antibody which specifically reacts, under immunologically reactive conditions, to a protein of the present invention. The antibody is allowed to bind to the protein under immunologically reactive conditions, and the presence of the bound antibody is detected directly or indirectly.

A. Non-Competitive Assay Formats

Immunoassays for detecting proteins of the present invention include competitive and noncompetitive formats. Noncompetitive immunoassays are assays in which the amount of captured analyte (i.e., a protein of the present invention) is directly
5 measured. In one preferred "sandwich" assay, for example, the capture agent (e.g., an antibody specifically reactive, under immunoreactive conditions, to a protein of the present invention) can be bound directly to a solid substrate where they are immobilized. These immobilized antibodies then capture the protein present in the test sample. The protein thus immobilized is then bound by a labeling agent, such as a second antibody
10 bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second can be modified with a detectable moiety, such as biotin, to which a third labeled molecule can specifically bind, such as enzyme-labeled streptavidin.

15

B. Competitive Assay Formats

In competitive assays, the amount of analyte present in the sample is measured indirectly by measuring the amount of an added (exogenous) analyte (e.g., a protein of the present invention) displaced (or competed away) from a capture agent (e.g., an
20 antibody specifically reactive, under immunoreactive conditions, to the protein) by the analyte present in the sample. In one competitive assay, a known amount of analyte is added to the sample and the sample is then contacted with a capture agent that specifically binds a protein of the present invention. The amount of protein bound to the capture agent is inversely proportional to the concentration of analyte present in the
25 sample.

In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of protein bound to the antibody may be determined either by measuring the amount of protein present in a protein/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of protein may
30 be detected by providing a labeled protein.

A hapten inhibition assay is another preferred competitive assay. In this assay a known analyte, (such as a protein of the present invention) is immobilized on a solid substrate. A known amount of antibody specifically reactive, under immunoreactive

conditions, to the protein is added to the sample, and the sample is then contacted with the immobilized protein. In this case, the amount of antibody bound to the immobilized protein is inversely proportional to the amount of protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized
5 fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

C. Generation of pooled antisera for use in immunoassays

10 A protein that specifically binds to or that is specifically immunoreactive with an antibody generated against a defined immunogen is determined in an immunoassay. The immunoassay uses a polyclonal antiserum which is raised to a polypeptide of the present invention (i.e., the immunogenic polypeptide). This antiserum is selected to have low crossreactivity against other proteins and any such crossreactivity is removed by
15 immunoabsorption prior to use in the immunoassay (e.g., by immunosorption of the antisera with a protein of different substrate specificity (e.g., a different enzyme) and/or a protein with the same substrate specificity but of a different form).

In order to produce antisera for use in an immunoassay, a polypeptide of the present invention is isolated as described herein. For example, recombinant protein can
20 be produced in a mammalian or other eukaryotic cell line. An inbred strain of mice is immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard mouse immunization protocol (see Harlow and Lane, above). Alternatively, a synthetic polypeptide derived from the sequences disclosed herein and conjugated to a carrier protein is used as an immunogen. Polyclonal sera are collected and titrated
25 against the immunogenic polypeptide in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against polypeptides of different forms or substrate specificity, using a competitive binding immunoassay such as the one described in Harlow and Lane, above, at pages 570-573.
30 Preferably, two or more distinct forms of polypeptides are used in this determination. These distinct types of polypeptides are used as competitors to identify antibodies which are specifically bound by the polypeptide being assayed for. The competitive

polypeptides can be produced as recombinant proteins and isolated using standard molecular biology and protein chemistry techniques as described herein.

Immunoassays in the competitive binding format are used for crossreactivity determinations. For example, the immunogenic polypeptide is immobilized to a solid support. Proteins added to the assay compete with the binding of the antisera to the immobilized antigen. The ability of the above proteins to compete with the binding of the antisera to the immobilized protein is compared to the immunogenic polypeptide. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% crossreactivity with a distinct form of a polypeptide are selected and pooled. The cross-reacting antibodies are then removed from the pooled antisera by immunoabsorbtion with a distinct form of a polypeptide.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described herein to compare a second "target" polypeptide to the immunogenic polypeptide. In order to make this comparison, the two polypeptides are each assayed at a wide range of concentrations and the amount of each polypeptide required to inhibit 50% of the binding of the antisera to the immobilized protein is determined using standard techniques. If the amount of the target polypeptide required is less than twice the amount of the immunogenic polypeptide that is required, then the target polypeptide is said to specifically bind to an antibody generated to the immunogenic protein. As a final determination of specificity, the pooled antisera is fully immunosorbed with the immunogenic polypeptide until no binding to the polypeptide used in the immunosorbtion is detectable. The fully immunosorbed antisera is then tested for reactivity with the test polypeptide. If no reactivity is observed, then the test polypeptide is specifically bound by the antisera elicited by the immunogenic protein.

D. Other Assay Formats

In a particularly preferred embodiment, Western blot (immunoblot) analysis is used to detect and quantify the presence of protein of the present invention in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind a protein of the present invention. The antibodies specifically bind to the protein on the solid support. These

antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the antibodies.

5

E. Quantification of Proteins.

The proteins of the present invention may be detected and quantified by any of a number of means well known to those of skill in the art. These include analytic biochemical methods such as electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, and the like, and various immunological methods such as fluid or gel precipitin reactions, immunodiffusion (single or double), immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, and the like.

15

F. Reduction of Non-Specific Binding

One of skill will appreciate that it is often desirable to reduce non-specific binding in immunoassays and during analyte purification. Where the assay involves an antigen, antibody, or other capture agent immobilized on a solid substrate, it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used.

20

25

G. Immunoassay Labels

The labeling agent can be, *e.g.*, a monoclonal antibody, a polyclonal antibody, a binding protein or complex, or a polymer such as an affinity matrix, carbohydrate or lipid. Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, radioisotopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Detection may proceed by any known method, such as immunoblotting, western analysis, gel-mobility shift assays, fluorescent *in situ* hybridization analysis (FISH), tracking of radioactive or

30

bioluminescent markers, nuclear magnetic resonance, electron paramagnetic resonance, stopped-flow spectroscopy, column chromatography, capillary electrophoresis, or other methods which track a molecule based upon an alteration in size and/or charge. The particular label or detectable group used in the assay is not a critical aspect of the invention. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads, fluorescent dyes, radiolabels, enzymes, and colorimetric labels or colored glass or plastic beads, as discussed for nucleic acid labels, above.

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on the sensitivity required, ease of conjugation of the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to an anti-ligand (*e.g.*, streptavidin) molecule which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. A number of ligands and anti-ligands can be used. Where a ligand has a natural anti-ligand, for example, biotin, thyroxine, and cortisol, it can be used in conjunction with the labeled, naturally occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an antibody.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*,

luminol. For a review of various labeling or signal producing systems which may be used, see, U.S. Patent No. 4,391,904, which is incorporated herein by reference.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation
5 counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence, *e.g.*, by microscopy, visual inspection, via photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by
10 providing appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance,
15 agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

20 Assays for Compounds that Modulate Enzymatic Activity or Expression

The present invention also provides means for identifying compounds that bind to (e.g., substrates), and/or increase or decrease (i.e., modulate) the enzymatic activity of, catalytically active polypeptides of the present invention. The method comprises
25 contacting a polypeptide of the present invention with a compound whose ability to bind to or modulate enzyme activity is to be determined. The polypeptide employed will have at least 20%, preferably at least 30% or 40%, more preferably at least 50% or 60%, and most preferably at least 70% or 80% of the specific activity of the native, full-length polypeptide of the present invention (e.g., enzyme). Generally, the polypeptide will be present in a range sufficient to determine the effect of the compound, typically about 1
30 nM to 10 μ M. Likewise, the compound will be present in a concentration of from about 1 nM to 10 μ M. Those of skill will understand that such factors as enzyme concentration, ligand concentrations (i.e., substrates, products, inhibitors, activators), pH, ionic strength, and temperature will be controlled so as to obtain useful kinetic data

and determine the presence or absence of a compound that binds or modulates polypeptide activity. Methods of measuring enzyme kinetics is well known in the art. See, e.g., Segel, *Biochemical Calculations*, 2nd ed., John Wiley and Sons, New York (1976).

5 Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

10 **Example 1**

 This example describes the construction cDNA libraries.

Total RNA Isolation

 Total RNA was isolated from corn tissues with TRIzol Reagent (Life Technology
15 Inc. Gaithersburg, MD) using a modification of the guanidine isothiocyanate/acid-phenol procedure described by Chomczynski and Sacchi (Chomczynski, P., and Sacchi, N. *Anal. Biochem.* 162, 156 (1987)). In brief, plant tissue samples were pulverized in liquid nitrogen before the addition of the TRIzol Reagent, and then were further homogenized with a mortar and pestle. Addition of chloroform followed by
20 centrifugation was conducted for separation of an aqueous phase and an organic phase. The total RNA was recovered by precipitation with isopropyl alcohol from the aqueous phase.

Poly(A)+ RNA Isolation

25 The selection of poly(A)+ RNA from total RNA was performed using PolyATact system (Promega Corporation, Madison, WI). In brief, biotinylated oligo(dT) primers were used to hybridize to the 3' poly(A) tails on mRNA. The hybrids were captured using streptavidin coupled to paramagnetic particles and a magnetic separation stand. The mRNA was washed at high stringent condition and eluted by RNase-free deionized
30 water.

cDNA Library Construction

cDNA synthesis was performed and unidirectional cDNA libraries were constructed using the SuperScript Plasmid System (Life Technology Inc. Gaithersburg, MD). The first strand of cDNA was synthesized by priming an oligo(dT) primer containing a Not I site. The reaction was catalyzed by SuperScript Reverse
5 Transcriptase II at 45°C. The second strand of cDNA was labeled with alpha-³²P-dCTP and a portion of the reaction was analyzed by agarose gel electrophoresis to determine cDNA sizes. cDNA molecules smaller than 500 base pairs and unligated adapters were removed by Sephacryl-S400 chromatography. The selected cDNA molecules were ligated into pSPORT1 vector in between of Not I and Sal I sites.

10

Example 2

This example describes cDNA sequencing and library subtraction.

Sequencing Template Preparation

Individual colonies were picked and DNA was prepared either by PCR with M13
15 forward primers and M13 reverse primers, or by plasmid isolation. All the cDNA clones were sequenced using M13 reverse primers.

Q-bot Subtraction Procedure

cDNA libraries subjected to the subtraction procedure were plated out on 22 x 22
20 cm² agar plate at density of about 3,000 colonies per plate. The plates were incubated in a 37°C incubator for 12-24 hours. Colonies were picked into 384-well plates by a robot colony picker, Q-bot (GENETIX Limited). These plates were incubated overnight at 37°C.

Once sufficient colonies were picked, they were pinned onto 22 x 22 cm² nylon
25 membranes using Q-bot. Each membrane contained 9,216 colonies or 36,864 colonies. These membranes were placed onto agar plate with appropriate antibiotic. The plates were incubated at 37°C for overnight.

After colonies were recovered on the second day, these filters were placed on
filter paper prewetted with denaturing solution for four minutes, then were incubated on
30 top of a boiling water bath for additional four minutes. The filters were then placed on filter paper prewetted with neutralizing solution for four minutes. After excess solution was removed by placing the filters on dry filter papers for one minute, the colony side of the filters were place into Proteinase K solution, incubated at 37°C for 40-50 minutes.

The filters were placed on dry filter papers to dry overnight. DNA was then cross-linked to nylon membrane by UV light treatment.

Colony hybridization was conducted as described by Sambrook, J., Fritsch, E.F. and Maniatis, T., (in *Molecular Cloning: A laboratory Manual*, 2nd Edition). The following probes were used in colony hybridization:

1. First strand cDNA from the same tissue as the library was made from to remove the most redundant clones.
2. 48-192 most redundant cDNA clones from the same library based on previous sequencing data.
3. 192 most redundant cDNA clones in the entire corn partial sequence database.
4. A Sal-A20 oligo nucleotide: TCG ACC CAC GCG TCC GAA AAA AAA AAA AAA AAA AAA, removes clones containing a poly A tail but no cDNA.
5. cDNA clones derived from rRNA.

The image of the autoradiography was scanned into computer and the signal intensity and cold colony addresses of each colony was analyzed. Re-arraying of cold-colonies from 384 well plates to 96 well plates was conducted using Q-bot.

Example 3

This example describes identification of the gene from a computer homology search. Gene identities were determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol.* 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm. The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics* 3:266-272) provided by the NCBI. In some cases, the sequencing data from two or more clones containing overlapping segments of DNA were used to construct contiguous DNA sequences.

The above examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising a member selected from the group consisting of:
 - 5 (a) a polynucleotide having at least 80% sequence identity, as determined by the BLAST 2.0 algorithm under default parameters, to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NOS: 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, and 58
 - (b) a polynucleotide encoding a polypeptide of SEQ ID NOS: 2, 6, 10, 14, 18,
10 22, 26, 30, 34, 38, 42, 46, 50, 54, and 58
 - (c) a polynucleotide amplified from a *Zea mays* nucleic acid library using primers which selectively hybridize, under stringent hybridization conditions, to loci within a polynucleotide selected from the group consisting of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57
 - 15 (d) a polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 2X SSC at 50°C, to a polynucleotide of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57
 - (e) a polynucleotide of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57
 - 20 (f) a polynucleotide which is complementary to a polynucleotide of (a), (b), (c), (d), or (e); and
 - (g) a polynucleotide comprising at least 25 contiguous nucleotides from a polynucleotide of (a), (b), (c), (d), (e), or (f).
- 25 2. A recombinant expression cassette, comprising a member of claim 1 operably linked, in sense or anti-sense orientation, to a promoter.
3. A host cell comprising the recombinant expression cassette of claim 2.
- 30 4. A transgenic plant comprising a recombinant expression cassette of claim 2.
5. The transgenic plant of claim 4, wherein the plant is a monocot.

6. The transgenic plant of claim 4, wherein the plant is selected from the group consisting of: maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, and millet.
- 5 7. A transgenic seed from the transgenic plant of claim 4.
8. A method of modulating the level of cellulose synthase in a plant cell capable of plant regeneration, comprising:
 - 10 (a) transforming the plant cell with a recombinant expression cassette comprising a cellulose synthase polynucleotide of claim 1 operably linked to a promoter;
 - (b) culturing the transformed plant cell; and
 - (c) inducing expression of said polynucleotide for a time sufficient to modulate the level of cellulose synthase in said transformed plant cell.
- 15 9. The method of claim 8, wherein a plant is regenerated from the transformed plant cell.
- 10 10. The method of claim 9, wherein the plant is selected from the group consisting of : maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, and millet.
- 20 11. The method of claim 8, wherein the promoter is a tissue-preferred promoter.
12. The method of claim 8, wherein the level of cellulose synthase is increased.
- 25 13. The method of claim 8 wherein the cell cycle polynucleotide is amplified from a *Zea mays* nucleic acid library using primers which selectively hybridize, under stringent hybridization conditions, to loci within a polynucleotide selected from the group consisting of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57.
- 30 14. The method of claim 8 wherein the cell cycle gene is selected from the group consisting of SEQ ID NOS: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57.

15. An isolated protein comprising a member selected from the group consisting of:
- (a) a polypeptide of at least 20 contiguous amino acids from a polypeptide of
SEQ ID NOS: 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, and 58
 - (b) a polypeptide of SEQ ID NOS: 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, 46,
5 50, 54, and 58
 - (c) a polypeptide having at least 80% sequence identity to, and having at least
one linear epitope in common with, a polypeptide of SEQ ID NOS: 2, 6, 10,
14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, and 58, wherein said sequence
identity is determined using BLAST 2.0 under default parameters; and,
 - 10 (d) a polypeptide encoded by a member of claim 1.

- 1 -

SEQUENCE LISTING

<110> Pioneer Hi-Bred International, Inc.

<120> Maize Cellulose Synthases and Uses
Thereof

<130> 0864-PCT

<150> 60/096,822

<151> August 17, 1998

<160> 60

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 3568

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (63)... (3237)

<400> 1

gtcgacccac gcgtccggag ctcgtcgctca tccgccgcga tggcgagcca gggccgaagc	60
cc atg gac cag cgg aac ggc cag gtg tgc cag att tgc ggc gac gac	107
Met Asp Gln Arg Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Asp	
1 5 10 15	
gtg ggg cgc aac ccc gac ggg gag cct ttc gtg gcc tgc aac gag tgc	155
Val Gly Arg Asn Pro Asp Gly Glu Pro Phe Val Ala Cys Asn Glu Cys	
20 25 30	
gcc ttc ccc atc tgc cgg gac tgc tac gag tac gag cgc cgc gag ggc	203
Ala Phe Pro Ile Cys Arg Asp Cys Tyr Glu Tyr Glu Arg Arg Glu Gly	
35 40 45	
acg cag aac tgc ccc cag tgc aag acc cgc ttc aag cgc ttc aag ggg	251
Thr Gln Asn Cys Pro Gln Cys Lys Thr Arg Phe Lys Arg Phe Lys Gly	
50 55 60	
tgc gcg cgc gtg ccc ggg gac gag gag gag gac ggc gtc gac gac ctg	299
Cys Ala Arg Val Pro Gly Asp Glu Glu Glu Asp Gly Val Asp Asp Leu	
65 70 75	
gag aac gag ttc aac tgg agc gac aag cac gac tcc cag tac ctc gcc	347
Glu Asn Glu Phe Asn Trp Ser Asp Lys His Asp Ser Gln Tyr Leu Ala	
80 85 90 95	
gag tcc atg ctc cac gcc cac atg agc tac ggc cgc ggc gcc gac ctc	395
Glu Ser Met Leu His Ala His Met Ser Tyr Gly Arg Gly Ala Asp Leu	
100 105 110	
gac ggc gtg ccg cag cca ttc cac ccc atc ccc aat gtt ccc ctc ctc	443

- 2 -

Asp Gly Val Pro Gln Pro Phe His Pro Ile Pro Asn Val Pro Leu Leu	
115 120 125	
acc aac gga cag atg gtc gat gac atc ccg ccg gac cag cac gcc ctt	491
Thr Asn Gly Gln Met Val Asp Asp Ile Pro Pro Asp Gln His Ala Leu	
130 135 140	
gtg ccc tcg ttc gtg ggt ggc ggg ggg aag agg att cac cct ctc ccg	539
Val Pro Ser Phe Val Gly Gly Gly Gly Lys Arg Ile His Pro Leu Pro	
145 150 155	
tac gcg gat ccc aac ctt cct gtg caa ccg agg tct atg gac cct tcc	587
Tyr Ala Asp Pro Asn Leu Pro Val Gln Pro Arg Ser Met Asp Pro Ser	
160 165 170 175	
aag gat ctc gcc gca tat ggc tac ggg agc gta gca tgg aag gag agg	635
Lys Asp Leu Ala Ala Tyr Gly Tyr Gly Ser Val Ala Trp Lys Glu Arg	
180 185 190	
atg gag agc tgg aag cag aag cag gag agg atg cac cag acg agg aac	683
Met Glu Ser Trp Lys Gln Lys Gln Glu Arg Met His Gln Thr Arg Asn	
195 200 205	
gat ggc ggc ggc gat gat ggt gat gat gca gat cta cca cta atg gat	731
Asp Gly Gly Gly Asp Asp Gly Asp Asp Ala Asp Leu Pro Leu Met Asp	
210 215 220	
gaa gct aga cag cca ttg tcc aga aag atc ccg ctt cct tca agc caa	779
Glu Ala Arg Gln Pro Leu Ser Arg Lys Ile Pro Leu Pro Ser Ser Gln	
225 230 235	
atc aac ccc tat agg atg att ata ata att ccg cta gtg gtt ttg tgt	827
Ile Asn Pro Tyr Arg Met Ile Ile Ile Ile Arg Leu Val Val Leu Cys	
240 245 250 255	
ttc ttc ttc cac tac cga gtg atg cat ccg gtg cct gat gca ttt gct	875
Phe Phe Phe His Tyr Arg Val Met His Pro Val Pro Asp Ala Phe Ala	
260 265 270	
tta tgg ctc ata tct gtg atc tgt gaa att tgg ttt gcc atg tct tgg	923
Leu Trp Leu Ile Ser Val Ile Cys Glu Ile Trp Phe Ala Met Ser Trp	
275 280 285	
att ctt gac cag ttt cca aag tgg ttt cct atc gag agg gaa acc tat	971
Ile Leu Asp Gln Phe Pro Lys Trp Phe Pro Ile Glu Arg Glu Thr Tyr	
290 295 300	
ctt gac cgg ctg agt tta agg ttt gac aag gaa ggg cat cct tct caa	1019
Leu Asp Arg Leu Ser Leu Arg Phe Asp Lys Glu Gly His Pro Ser Gln	
305 310 315	
ctc gcc cct gtt gat ttc ttt gtc agt acg gtt gat ccc ttg aag gaa	1067
Leu Ala Pro Val Asp Phe Phe Val Ser Thr Val Asp Pro Leu Lys Glu	
320 325 330 335	
cct cca ttg gtc act gct aat act gtt cta tct atc ctt tcg gtg gat	1115
Pro Pro Leu Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ser Val Asp	
340 345 350	

- 3 -

tat cca gtt gat aag gtt tca tgc tac gtt tct gat gat ggt gct gcc Tyr Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala 355 360 365	1163
atg ctg aca ttt gaa gca ttg tct gaa aca tct gaa ttt gca aag aaa Met Leu Thr Phe Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala Lys Lys 370 375 380	1211
tgg gtt cct ttc tgc aaa aga tat agc ctt gag cct cgt gct cca gag Trp Val Pro Phe Cys Lys Arg Tyr Ser Leu Glu Pro Arg Ala Pro Glu 385 390 395	1259
tgg tac ttc caa cag aag ata gac tac ctg aaa gac aag gtg gcg cca Trp Tyr Phe Gln Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Ala Pro 400 405 410 415	1307
aac ttt gtt aga gaa cgg aga gca atg aag aga gag tat gag gaa ttc Asn Phe Val Arg Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe 420 425 430	1355
aag gtc aga atc aat gcc ttg gtt gct aaa gcc caa aag gtt cct gag Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu 435 440 445	1403
gaa gga tgg aca atg cag gat gga act cca tgg ccc gga aat aat gtc Glu Gly Trp Thr Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Val 450 455 460	1451
cgt gat cat cct gga atg att cag gtt ttc ctt ggt caa agt ggt ggc Arg Asp His Pro Gly Met Ile Gln Val Phe Leu Gly Gln Ser Gly Gly 465 470 475	1499
cat gat gtg gaa gga aat gag ctg cct cga ttg gtt tat gtt tca aga His Asp Val Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg 480 485 490 495	1547
gaa aaa cgg cca ggc tac aac cat cac aag aag gct ggt gct atg aat Glu Lys Arg Pro Gly Tyr Asn His His Lys Lys Ala Gly Ala Met Asn 500 505 510	1595
gca ttg gtc cga gtc tct gct gta cta act aat gct cct tat ttg ctg Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Ala Pro Tyr Leu Leu 515 520 525	1643
aac ttg gat tgt gat cac tat atc aat aat agt aag gct ata aag gaa Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Ile Lys Glu 530 535 540	1691
gca atg tgt ttt atg atg gat cct ttg ctt gga aag aaa gtt tgc tat Ala Met Cys Phe Met Met Asp Pro Leu Leu Gly Lys Lys Val Cys Tyr 545 550 555	1739
gtg cag ttt cct caa aga ttt gat ggg att gat cgc cat gat cga tat Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr 560 565 570 575	1787
gct aac aga aat gtt gtc ttt ttc gat atc aac atg aaa ggt ttg gat	1835

- 4 -

Ala Asn Arg Asn Val Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp	
580 585 590	
ggt atc cag ggc cca att tat gtg ggt act gga tgt gtc ttc aga agg	1883
Gly Ile Gln Gly Pro Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg	
595 600 605	
cag gca tta tat ggc tac gat gct ccc aaa aca aag aag cca cca tca	1931
Gln Ala Leu Tyr Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro Pro Ser	
610 615 620	
aga act tgc aac tgc tgg cca aag tgg tgc att tgc tgt tgc tgt ttt	1979
Arg Thr Cys Asn Cys Trp Pro Lys Trp Cys Ile Cys Cys Cys Cys Phe	
625 630 635	
ggt aac agg aag acc aag aag aag acc aag acc tct aaa cct aaa ttt	2027
Gly Asn Arg Lys Thr Lys Lys Lys Thr Lys Thr Ser Lys Pro Lys Phe	
640 645 650 655	
gag aag ata aag aaa ctt ttt aag aaa aag gaa aat caa gcc cct gca	2075
Glu Lys Ile Lys Lys Leu Phe Lys Lys Lys Glu Asn Gln Ala Pro Ala	
660 665 670	
tat gct ctt ggt gaa att gat gaa gcc gct cca gga gct gaa aat gaa	2123
Tyr Ala Leu Gly Glu Ile Asp Glu Ala Ala Pro Gly Ala Glu Asn Glu	
675 680 685	
aag gct agt att gta aat caa cag aag ttg gaa aag aaa ttt ggc cag	2171
Lys Ala Ser Ile Val Asn Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln	
690 695 700	
tct tca gtt ttt gtt gca tcc aca ctt ctt gag aat ggt gga acc ctg	2219
Ser Ser Val Phe Val Ala Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu	
705 710 715	
aag agt gcc agt cca gct tct ctt ctg aag gaa gct ata cat gtc atc	2267
Lys Ser Ala Ser Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile	
720 725 730 735	
agt tgt gga tat gaa gac aaa aca ggc tgg gga aaa gat att ggt tgg	2315
Ser Cys Gly Tyr Glu Asp Lys Thr Gly Trp Gly Lys Asp Ile Gly Trp	
740 745 750	
att tat gga tca gtc aca gaa gat att ctt act ggg ttt aag atg cac	2363
Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His	
755 760 765	
tgc cat ggt tgg cgg tca att tac tgc ata cct aaa cgg gcc gcc ttc	2411
Cys His Gly Trp Arg Ser Ile Tyr Cys Ile Pro Lys Arg Ala Ala Phe	
770 775 780	
aaa ggt tcc gca cct ctc aat ctt tcc gat cgt ttt cac cag gtt ctt	2459
Lys Gly Ser Ala Pro Leu Asn Leu Ser Asp Arg Phe His Gln Val Leu	
785 790 795	
cgg tgg gct ctt ggt tca att gaa att ttg ttc agc aac cac tgc cct	2507
Arg Trp Ala Leu Gly Ser Ile Glu Ile Leu Phe Ser Asn His Cys Pro	
800 805 810 815	

- 5 -

ctc tgg tat ggg tat ggt ggt gga cta aag ttc ctg gaa agg ttt tcg Leu Trp Tyr Gly Tyr Gly Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser 820 825 830	2555
tac att aac tcc atc gta tac cct tgg aca tct atc ccg ctc ttg gcc Tyr Ile Asn Ser Ile Val Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala 835 840 845	2603
tat tgc aca ttg cct gcc atc tgc ttg ctg aca ggg aaa ttt atc acg Tyr Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr 850 855 860	2651
cca gag ctt aac aat gtt gcc agc ctc tgg ttc atg tca ctt ttc atc Pro Glu Leu Asn Asn Val Ala Ser Leu Trp Phe Met Ser Leu Phe Ile 865 870 875	2699
tgc att ttt gct acg agc atc ctg gaa atg aga tgg agt ggt gta ggc Cys Ile Phe Ala Thr Ser Ile Leu Glu Met Arg Trp Ser Gly Val Gly 880 885 890 895	2747
atc gat gac tgg tgg aga aac gag cag ttt tgg gtc att gga ggc gtg Ile Asp Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val 900 905 910	2795
tct tca cat ctc ttt gct gtg ttc cag gga ctc ctc aag gtc ata gct Ser Ser His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Ile Ala 915 920 925	2843
ggt gta gac acg agc ttc act gtg aca tcc aag ggc gga gac gac gag Gly Val Asp Thr Ser Phe Thr Val Thr Ser Lys Gly Gly Asp Asp Glu 930 935 940	2891
gag ttc tca gag ctg tac aca ttc aaa tgg acg acc ctt ctg ata cct Glu Phe Ser Glu Leu Tyr Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro 945 950 955	2939
ccg aca acc ctg ctc cta ctg aac ttc att gga gtg gta gct ggc atc Pro Thr Thr Leu Leu Leu Leu Asn Phe Ile Gly Val Val Ala Gly Ile 960 965 970 975	2987
tcc aat gcg atc aac aac gga tat gaa tca tgg ggc ccc ctg ttc ggg Ser Asn Ala Ile Asn Asn Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly 980 985 990	3035
aag ctc ttc ttt gca ttt tgg gtg atc gtc cat ctt tac ccg ttc ctc Lys Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu 995 1000 1005	3083
aag ggt ctg gtt ggg agg cag aac agg acg cca acg att gtc att gtc Lys Gly Leu Val Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val 1010 1015 1020	3131
tgg tcc atc ctc ctg gct tcg atc ttc tcg ctg ctt tgg gtc cgg atc Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile 1025 1030 1035	3179
gac ccg ttc ctt gcg aag gat gat ggt ccc ctg ttg gag gag tgt ggt	3227

- 6 -

Asp Pro Phe Leu Ala Lys Asp Asp Gly Pro Leu Leu Glu Glu Cys Gly
 1040 1045 1050 1055

ctg gat tgc a actaggaggt cagcacgtgg acttccccgt cagtgtgtgg 3277
 Leu Asp Cys

tcgaagaagt atttttgcag atgttttgtg cccatatttc tttactcaat tttgtccct 3337
 ctgtagattg aaacaagggg tgaaggggaa aaaaagtact tgtatttctt ttgttccatg 3397
 gtggtggtgg tgggtgggagg ctcagcctcg tgagtgcatt attgggcaaa ccggaggttg 3457
 cggcaacctt gtgcagttcg tccacgaatn tactagggat gatcgcgacc aatcaatcaa 3517
 tcgatgaccg agttcaattg ttcaaaaaaa aaaaaaaaaa agggcgggccg c 3568

<210> 2

<211> 1059

<212> PRT

<213> Zea mays

<400> 2

Met Asp Gln Arg Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Asp Val
 1 5 10 15
 Gly Arg Asn Pro Asp Gly Glu Pro Phe Val Ala Cys Asn Glu Cys Ala
 20 25 30
 Phe Pro Ile Cys Arg Asp Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Thr
 35 40 45
 Gln Asn Cys Pro Gln Cys Lys Thr Arg Phe Lys Arg Phe Lys Gly Cys
 50 55 60
 Ala Arg Val Pro Gly Asp Glu Glu Glu Asp Gly Val Asp Asp Leu Glu
 65 70 75 80
 Asn Glu Phe Asn Trp Ser Asp Lys His Asp Ser Gln Tyr Leu Ala Glu
 85 90 95
 Ser Met Leu His Ala His Met Ser Tyr Gly Arg Gly Ala Asp Leu Asp
 100 105 110
 Gly Val Pro Gln Pro Phe His Pro Ile Pro Asn Val Pro Leu Leu Thr
 115 120 125
 Asn Gly Gln Met Val Asp Asp Ile Pro Pro Asp Gln His Ala Leu Val
 130 135 140
 Pro Ser Phe Val Gly Gly Gly Gly Lys Arg Ile His Pro Leu Pro Tyr
 145 150 155 160
 Ala Asp Pro Asn Leu Pro Val Gln Pro Arg Ser Met Asp Pro Ser Lys
 165 170 175
 Asp Leu Ala Ala Tyr Gly Tyr Gly Ser Val Ala Trp Lys Glu Arg Met
 180 185 190
 Glu Ser Trp Lys Gln Lys Gln Glu Arg Met His Gln Thr Arg Asn Asp
 195 200 205
 Gly Gly Gly Asp Asp Gly Asp Asp Ala Asp Leu Pro Leu Met Asp Glu
 210 215 220
 Ala Arg Gln Pro Leu Ser Arg Lys Ile Pro Leu Pro Ser Ser Gln Ile
 225 230 235 240
 Asn Pro Tyr Arg Met Ile Ile Ile Ile Arg Leu Val Val Leu Cys Phe
 245 250 255
 Phe Phe His Tyr Arg Val Met His Pro Val Pro Asp Ala Phe Ala Leu
 260 265 270
 Trp Leu Ile Ser Val Ile Cys Glu Ile Trp Phe Ala Met Ser Trp Ile
 275 280 285
 Leu Asp Gln Phe Pro Lys Trp Phe Pro Ile Glu Arg Glu Thr Tyr Leu
 290 295 300
 Asp Arg Leu Ser Leu Arg Phe Asp Lys Glu Gly His Pro Ser Gln Leu

- 7 -

305 310 315 320
 Ala Pro Val Asp Phe Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro
 325 330 335
 Pro Leu Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr
 340 345 350
 Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met
 355 360 365
 Leu Thr Phe Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala Lys Lys Trp
 370 375 380
 Val Pro Phe Cys Lys Arg Tyr Ser Leu Glu Pro Arg Ala Pro Glu Trp
 385 390 395 400
 Tyr Phe Gln Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Ala Pro Asn
 405 410 415
 Phe Val Arg Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys
 420 425 430
 Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu
 435 440 445
 Gly Trp Thr Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Val Arg
 450 455 460
 Asp His Pro Gly Met Ile Gln Val Phe Leu Gly Gln Ser Gly Gly His
 465 470 475 480
 Asp Val Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu
 485 490 495
 Lys Arg Pro Gly Tyr Asn His His Lys Lys Ala Gly Ala Met Asn Ala
 500 505 510
 Leu Val Arg Val Ser Ala Val Leu Thr Asn Ala Pro Tyr Leu Leu Asn
 515 520 525
 Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Ile Lys Glu Ala
 530 535 540
 Met Cys Phe Met Met Asp Pro Leu Leu Gly Lys Lys Val Cys Tyr Val
 545 550 555 560
 Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr Ala
 565 570 575
 Asn Arg Asn Val Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly
 580 585 590
 Ile Gln Gly Pro Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg Gln
 595 600 605
 Ala Leu Tyr Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro Pro Ser Arg
 610 615 620
 Thr Cys Asn Cys Trp Pro Lys Trp Cys Ile Cys Cys Cys Phe Gly
 625 630 635 640
 Asn Arg Lys Thr Lys Lys Lys Thr Lys Thr Ser Lys Pro Lys Phe Glu
 645 650 655
 Lys Ile Lys Lys Leu Phe Lys Lys Lys Glu Asn Gln Ala Pro Ala Tyr
 660 665 670
 Ala Leu Gly Glu Ile Asp Glu Ala Ala Pro Gly Ala Glu Asn Glu Lys
 675 680 685
 Ala Ser Ile Val Asn Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln Ser
 690 695 700
 Ser Val Phe Val Ala Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu Lys
 705 710 715 720
 Ser Ala Ser Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser
 725 730 735
 Cys Gly Tyr Glu Asp Lys Thr Gly Trp Gly Lys Asp Ile Gly Trp Ile
 740 745 750
 Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys
 755 760 765
 His Gly Trp Arg Ser Ile Tyr Cys Ile Pro Lys Arg Ala Ala Phe Lys

- 8 -

```

      770              775              780
Gly Ser Ala Pro Leu Asn Leu Ser Asp Arg Phe His Gln Val Leu Arg
785              790              795              800
Trp Ala Leu Gly Ser Ile Glu Ile Leu Phe Ser Asn His Cys Pro Leu
      805              810              815
Trp Tyr Gly Tyr Gly Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser Tyr
      820              825              830
Ile Asn Ser Ile Val Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala Tyr
      835              840              845
Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr Pro
      850              855              860
Glu Leu Asn Asn Val Ala Ser Leu Trp Phe Met Ser Leu Phe Ile Cys
865              870              875              880
Ile Phe Ala Thr Ser Ile Leu Glu Met Arg Trp Ser Gly Val Gly Ile
      885              890              895
Asp Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser
      900              905              910
Ser His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Ile Ala Gly
      915              920              925
Val Asp Thr Ser Phe Thr Val Thr Ser Lys Gly Gly Asp Asp Glu Glu
      930              935              940
Phe Ser Glu Leu Tyr Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro
945              950              955              960
Thr Thr Leu Leu Leu Leu Asn Phe Ile Gly Val Val Ala Gly Ile Ser
      965              970              975
Asn Ala Ile Asn Asn Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly Lys
      980              985              990
Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys
      995              1000              1005
Gly Leu Val Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp
      1010              1015              1020
Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp
1025              1030              1035              1040
Pro Phe Leu Ala Lys Asp Asp Gly Pro Leu Leu Glu Glu Cys Gly Leu
      1045              1050              1055
Asp Cys Asn

```

<210> 3

<211> 25

<212> DNA

<213> Zea mays

<400> 3

atggaccagc ggaacggcca ggtgt
25

<210> 4

<211> 25

<212> DNA

<213> Zea mays

<400> 4

ctagttgcaa tccagaccac actcc
25

<210> 5

<211> 3773

- 9 -

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (338) ... (3566)

<400> 5

```

gtcgacccac gcgtccgcta ggatcaaac cgtctcgccg ctgcaataat cttttgtcaa      60
ttcttaatcc ctcgcgtcga cagcgacagc ggaaccaact cacgttgccg cggcttcctc     120
catcgggtgcg gtgccctgtc cttttctctc gtccctcctc ccccggtata gttaagcccc     180
gccccgctac tactactact agcagcagca gcgctctcgc agcgggagat gcggtgttga     240
tccgtgcccc gctcggatct cgggactggg gccggctctg cccaggcccc aggctccagg     300
ccagctccct cgacgtttct cggcgagctc gcttgcc atg gag ggc gac gcg gac     355
                               Met Glu Gly Asp Ala Asp
                               1           5

ggc gtg aag tcg ggg agg cgc ggt ggc gga cag gtg tgc cag atc tgc      403
Gly Val Lys Ser Gly Arg Arg Gly Gly Gly Gln Val Cys Gln Ile Cys
           10           15           20

ggc gac ggc gtg ggc acc acg gcg gag ggg gac gtc ttc gcc gcc tgc      451
Gly Asp Gly Val Gly Thr Thr Ala Glu Gly Asp Val Phe Ala Ala Cys
           25           30           35

gac gtc tgc ggg ttt ccg gtg tgc cgc ccc tgc tac gag tac gag cgc      499
Asp Val Cys Gly Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg
           40           45           50

aag gac ggc acg cag gcg tgc ccc cag tgc aag acc aag tac aag cgc      547
Lys Asp Gly Thr Gln Ala Cys Pro Gln Cys Lys Thr Lys Tyr Lys Arg
           55           60           65           70

cac aag ggg agc ccg gcg atc cgt ggg gag gaa gga gac gac act gat      595
His Lys Gly Ser Pro Ala Ile Arg Gly Glu Glu Gly Asp Asp Thr Asp
           75           80           85

gcc gat agc gac ttc aat tac ctt gca tct ggc aat gag gac cag aag      643
Ala Asp Ser Asp Phe Asn Tyr Leu Ala Ser Gly Asn Glu Asp Gln Lys
           90           95           100

cag aag att gcc gac aga atg cgc agc tgg cgc atg aac gtt ggg ggc      691
Gln Lys Ile Ala Asp Arg Met Arg Ser Trp Arg Met Asn Val Gly Gly
           105           110           115

agc ggg gat gtt ggt cgc ccc aag tat gac agt ggc gag atc ggg ctt      739
Ser Gly Asp Val Gly Arg Pro Lys Tyr Asp Ser Gly Glu Ile Gly Leu
           120           125           130

acc aag tat gac agt ggc gag att cct cgg gga tac atc cca tca gtc      787
Thr Lys Tyr Asp Ser Gly Glu Ile Pro Arg Gly Tyr Ile Pro Ser Val
           135           140           145           150

act aac agc cag atc tca gga gaa atc cct ggt gct tcc cct gac cat      835
Thr Asn Ser Gln Ile Ser Gly Glu Ile Pro Gly Ala Ser Pro Asp His
           155           160           165

cat atg atg tcc cca act ggg aac att ggc aag cgt gct cca ttt ccc      883

```

- 10 -

His Met Met Ser Pro Thr Gly Asn Ile Gly Lys Arg Ala Pro Phe Pro	
170 175 180	
tat gtg aac cat tcg cca aat ccg tca agg gag ttc tct ggt agc att	931
Tyr Val Asn His Ser Pro Asn Pro Ser Arg Glu Phe Ser Gly Ser Ile	
185 190 195	
ggg aat gtt gcc tgg aaa gag agg gtt gat ggc tgg aaa atg aag cag	979
Gly Asn Val Ala Trp Lys Glu Arg Val Asp Gly Trp Lys Met Lys Gln	
200 205 210	
gac aag ggg acg att ccc atg acg aat ggc aca agc att gct ccc tct	1027
Asp Lys Gly Thr Ile Pro Met Thr Asn Gly Thr Ser Ile Ala Pro Ser	
215 220 225 230	
gag ggt cgg ggt gtt ggt gat att gat gca tca act gat tac aac atg	1075
Glu Gly Arg Gly Val Gly Asp Ile Asp Ala Ser Thr Asp Tyr Asn Met	
235 240 245	
gaa gat gcc tta ttg aac gac gaa act cga cag cct cta tct agg aaa	1123
Glu Asp Ala Leu Leu Asn Asp Glu Thr Arg Gln Pro Leu Ser Arg Lys	
250 255 260	
gtt cca ctt cct tcc tcc agg ata aat cca tac agg atg gtc att gtg	1171
Val Pro Leu Pro Ser Ser Arg Ile Asn Pro Tyr Arg Met Val Ile Val	
265 270 275	
ctg cga ttg att gtt cta agc atc ttc ttg cac tac cgt atc aca aat	1219
Leu Arg Leu Ile Val Leu Ser Ile Phe Leu His Tyr Arg Ile Thr Asn	
280 285 290	
cct gtg cgc aat gca tac cca tta tgg ctt cta tct gtt ata tgt gag	1267
Pro Val Arg Asn Ala Tyr Pro Leu Trp Leu Leu Ser Val Ile Cys Glu	
295 300 305 310	
atc tgg ttt gct ctt tcg tgg ata ttg gat cag ttc cct aag tgg ttt	1315
Ile Trp Phe Ala Leu Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Phe	
315 320 325	
cca atc aac cgg gag acg tac ctt gat agg ctg gca tta agg tat gac	1363
Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu Arg Tyr Asp	
330 335 340	
cgg gaa ggt gag cca tct cag ttg gct gct gtt gac att ttc gtc agt	1411
Arg Glu Gly Glu Pro Ser Gln Leu Ala Ala Val Asp Ile Phe Val Ser	
345 350 355	
aca gtc gac cca atg aag gag cct cct ctt gtc act gcc aat acc gtg	1459
Thr Val Asp Pro Met Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val	
360 365 370	
cta tcc att ctt gct gtg gat tac cct gtg gat aag gtc tct tgc tat	1507
Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser Cys Tyr	
375 380 385 390	
gta tct gat gat gga gct gcg atg ctg aca ttt gat gca cta gct gag	1555
Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Asp Ala Leu Ala Glu	
395 400 405	

- 11 -

act tca gag ttt gct aga aaa tgg gta cca ttt gtt aag aag tac aac Thr Ser Glu Phe Ala Arg Lys Trp Val Pro Phe Val Lys Lys Tyr Asn 410 415 420	1603
att gaa cct aga gct cct gaa tgg tac ttc tcc cag aaa att gat tac Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Ser Gln Lys Ile Asp Tyr 425 430 435	1651
ttg aag gac aaa gtg cac cct tca ttt gtt aaa gac cgc cgg gcc atg Leu Lys Asp Lys Val His Pro Ser Phe Val Lys Asp Arg Arg Ala Met 440 445 450	1699
aag aga gaa tat gaa gaa ttc aaa gtt agg gta aat ggc ctt gtt gct Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Val Asn Gly Leu Val Ala 455 460 465 470	1747
aag gca cag aaa gtt cct gag gaa gga tgg atc atg caa gat ggc aca Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Ile Met Gln Asp Gly Thr 475 480 485	1795
cca tgg cca gga aac aat acc mgg gac cat cct gga atg att cag gtt Pro Trp Pro Gly Asn Asn Thr Xaa Asp His Pro Gly Met Ile Gln Val 490 495 500	1843
ttc ctt ggt cac agt ggt ggc ctt gat act gag ggc aat gag cta ccc Phe Leu Gly His Ser Gly Gly Leu Asp Thr Glu Gly Asn Glu Leu Pro 505 510 515	1891
cgt ttg gtc tat gtt tct cgt gaa aag cgt cct gga ttc cag cat cac Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln His His 520 525 530	1939
aag aaa gct ggt gcc atg aat gct ctt gtt cgt gtc tca gct gtg ctt Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val Leu 535 540 545 550	1987
acc aat gga caa tac atg ttg aat ctt gat tgt gat cac tac att aac Thr Asn Gly Gln Tyr Met Leu Asn Leu Asp Cys Asp His Tyr Ile Asn 555 560 565	2035
aac agt aag gct ctc agg gaa gct atg tgc ttc ctt atg gac cct aac Asn Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Leu Met Asp Pro Asn 570 575 580	2083
cta gga agg agt gtc tgc tac gtc cag ttt ccc cag aga ttc gat ggc Leu Gly Arg Ser Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly 585 590 595	2131
att gac agg aat gat cga tat gcc aac agg aac acc gtg ttt ttc gat Ile Asp Arg Asn Asp Arg Tyr Ala Asn Arg Asn Thr Val Phe Phe Asp 600 605 610	2179
att aac ttg aga ggt ctt gat ggc atc caa gga cca gtt tat gtc gga Ile Asn Leu Arg Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr Val Gly 615 620 625 630	2227
act ggc tgt gtt ttc aac cga aca gct cta tat ggt tat gag ccc cca	2275

- 12 -

Thr Gly Cys Val Phe Asn Arg Thr Ala Leu Tyr Gly Tyr Glu Pro Pro	
635 640 645	
att aag cag aag aag ggt ggt ttc ttg tca tca cta tgt ggc ggt agg	2323
Ile Lys Gln Lys Lys Gly Gly Phe Leu Ser Ser Leu Cys Gly Gly Arg	
650 655 660	
aag aag gca agc aaa tca aag aag ggc tcg gac aag aag aag tcg cag	2371
Lys Lys Ala Ser Lys Ser Lys Lys Gly Ser Asp Lys Lys Lys Ser Gln	
665 670 675	
aag cat gtg gac agt tct gtg cca gta ttc aac ctt gaa gat ata gag	2419
Lys His Val Asp Ser Ser Val Pro Val Phe Asn Leu Glu Asp Ile Glu	
680 685 690	
gag gga gtt gaa ggc gct gga ttt gac gac gag aaa tca ctt ctt atg	2467
Glu Gly Val Glu Gly Ala Gly Phe Asp Asp Glu Lys Ser Leu Leu Met	
695 700 705 710	
tct caa atg agc ctg gag aag aga ttt ggc cag tcc gca gcg ttt gtt	2515
Ser Gln Met Ser Leu Glu Lys Arg Phe Gly Gln Ser Ala Ala Phe Val	
715 720 725	
gcc tcc act ctg atg gag tat ggt ggt gtt cct cag tcc gca act ccg	2563
Ala Ser Thr Leu Met Glu Tyr Gly Gly Val Pro Gln Ser Ala Thr Pro	
730 735 740	
gag tct ctt ctg aaa gaa gct atc cat gtt ata agc tgt ggc tat gag	2611
Glu Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu	
745 750 755	
gac aag act gaa tgg gga act gag atc ggg tgg atc tac ggt tct gtg	2659
Asp Lys Thr Glu Trp Gly Thr Glu Ile Gly Trp Ile Tyr Gly Ser Val	
760 765 770	
aca gaa gac att ctc acc gga ttc aag atg cac gcg cga ggc tgg cgg	2707
Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Arg	
775 780 785 790	
tcg atc tac tgc atg ccc aag cgg cca gct ttc aag ggg tct gcc ccc	2755
Ser Ile Tyr Cys Met Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro	
795 800 805	
atc aat ctt tcg gac cgt ctg aac cag gtg ctc cgg tgg gct ctt ggg	2803
Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly	
810 815 820	
tcc gtg gag atc ctc ttc agc cgg cac tgc ccc ctg tgg tac ggc tac	2851
Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Leu Trp Tyr Gly Tyr	
825 830 835	
gga ggg cgg ctc aag ttc ctg gag aga ttc gcg tac atc aac acc acc	2899
Gly Gly Arg Leu Lys Phe Leu Glu Arg Phe Ala Tyr Ile Asn Thr Thr	
840 845 850	
atc tac ccg ctc acg tcc atc ccg ctt ctc atc tac tgc atc ctg ccc	2947
Ile Tyr Pro Leu Thr Ser Ile Pro Leu Leu Ile Tyr Cys Ile Leu Pro	
855 860 865 870	

- 13 -

gcc atc tgt ctg ctc acc gga aag ttc atc att cca gag atc agc aac Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Ile Pro Glu Ile Ser Asn 875 880 885	2995
ttc gcc agc atc tgg ttc atc tcc ctc ttc atc tcg atc ttc gcc acg Phe Ala Ser Ile Trp Phe Ile Ser Leu Phe Ile Ser Ile Phe Ala Thr 890 895 900	3043
ggc atc ctg gag atg agg tgg agc ggg gtg ggc atc gac gag tgg tgg Gly Ile Leu Glu Met Arg Trp Ser Gly Val Gly Ile Asp Glu Trp Trp 905 910 915	3091
agg aac gag cag ttc tgg gtg atc ggg ggc atc tcc gcg cac ctc ttc Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Ile Ser Ala His Leu Phe 920 925 930	3139
gcc gtg ttc cag ggc ctg ctc aag gtg ctg gcc ggc atc gac acc aac Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn 935 940 945 950	3187
ttc acc gtc acc tcc aag gcc tcg gac gag gac ggc gac ttc gcg gag Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp Phe Ala Glu 955 960 965	3235
ctg tac atg ttc aag tgg acg acg ctc ctg atc ccg ccc acc acc atc Leu Tyr Met Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Ile 970 975 980	3283
ctg atc atc aac ctg gtc ggc gtc gtc gcc ggc atc tcc tac gcc atc Leu Ile Ile Asn Leu Val Gly Val Val Ala Gly Ile Ser Tyr Ala Ile 985 990 995	3331
aac agc gga tac cag tcg tgg ggc ccg ctc ttc ggc aag ctc ttc ttc Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe 1000 1005 1010	3379
gcc ttc tgg gtc atc gtc cac ctg tac ccg ttc ctc aag ggc ctc atg Ala Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Met 1015 1020 1025 1030	3427
ggc agg cag aac cgc acc ccg acc atc gtc gtc gtc tgg gcc atc ctg Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Val Val Trp Ala Ile Leu 1035 1040 1045	3475
ctg gcg tcc atc ttc tcc ttg ctg tgg gtt cgc atc gac ccc ttc acc Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Thr 1050 1055 1060	3523
acc cgc gtc act ggc ccg gat acc cag acg tgt ggc atc aac t Thr Arg Val Thr Gly Pro Asp Thr Gln Thr Cys Gly Ile Asn 1065 1070 1075	3566
gctaggggaag tggaagggttt gtacttttgta gaaacggagg aataccacgt gccatctgtt gtctgttaag ttatatatat ataagcagca agtggcggtta ttacagcta cgtacagacc agtggatatt gtttaccaca aagttttact tgtgttaata tgcattcttt tgttgatata aaaaaaaaa aaaaaaaggg cggccgc	3626 3686 3746 3773

- 14 -

<210> 6
 <211> 1077
 <212> PRT
 <213> Zea mays

<400> 6

Met Glu Gly Asp Ala Asp Gly Val Lys Ser Gly Arg Arg Gly Gly Gly
 1 5 10 15
 Gln Val Cys Gln Ile Cys Gly Asp Gly Val Gly Thr Thr Ala Glu Gly
 20 25 30
 Asp Val Phe Ala Ala Cys Asp Val Cys Gly Phe Pro Val Cys Arg Pro
 35 40 45
 Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Thr Gln Ala Cys Pro Gln Cys
 50 55 60
 Lys Thr Lys Tyr Lys Arg His Lys Gly Ser Pro Ala Ile Arg Gly Glu
 65 70 75 80
 Glu Gly Asp Asp Thr Asp Ala Asp Ser Asp Phe Asn Tyr Leu Ala Ser
 85 90 95
 Gly Asn Glu Asp Gln Lys Gln Lys Ile Ala Asp Arg Met Arg Ser Trp
 100 105 110
 Arg Met Asn Val Gly Gly Ser Gly Asp Val Gly Arg Pro Lys Tyr Asp
 115 120 125
 Ser Gly Glu Ile Gly Leu Thr Lys Tyr Asp Ser Gly Glu Ile Pro Arg
 130 135 140
 Gly Tyr Ile Pro Ser Val Thr Asn Ser Gln Ile Ser Gly Glu Ile Pro
 145 150 155 160
 Gly Ala Ser Pro Asp His His Met Met Ser Pro Thr Gly Asn Ile Gly
 165 170 175
 Lys Arg Ala Pro Phe Pro Tyr Val Asn His Ser Pro Asn Pro Ser Arg
 180 185 190
 Glu Phe Ser Gly Ser Ile Gly Asn Val Ala Trp Lys Glu Arg Val Asp
 195 200 205
 Gly Trp Lys Met Lys Gln Asp Lys Gly Thr Ile Pro Met Thr Asn Gly
 210 215 220
 Thr Ser Ile Ala Pro Ser Glu Gly Arg Gly Val Gly Asp Ile Asp Ala
 225 230 235 240
 Ser Thr Asp Tyr Asn Met Glu Asp Ala Leu Leu Asn Asp Glu Thr Arg
 245 250 255
 Gln Pro Leu Ser Arg Lys Val Pro Leu Pro Ser Ser Arg Ile Asn Pro
 260 265 270
 Tyr Arg Met Val Ile Val Leu Arg Leu Ile Val Leu Ser Ile Phe Leu
 275 280 285
 His Tyr Arg Ile Thr Asn Pro Val Arg Asn Ala Tyr Pro Leu Trp Leu
 290 295 300
 Leu Ser Val Ile Cys Glu Ile Trp Phe Ala Leu Ser Trp Ile Leu Asp
 305 310 315 320
 Gln Phe Pro Lys Trp Phe Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg
 325 330 335
 Leu Ala Leu Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Ala
 340 345 350
 Val Asp Ile Phe Val Ser Thr Val Asp Pro Met Lys Glu Pro Pro Leu
 355 360 365
 Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val
 370 375 380
 Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr
 385 390 395 400
 Phe Asp Ala Leu Ala Glu Thr Ser Glu Phe Ala Arg Lys Trp Val Pro
 405 410 415

- 15 -

Phe Val Lys Lys Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe
 420 425 430
 Ser Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val His Pro Ser Phe Val
 435 440 445
 Lys Asp Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg
 450 455 460
 Val Asn Gly Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp
 465 470 475 480
 Ile Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Thr Xaa Asp His
 485 490 495
 Pro Gly Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr
 500 505 510
 Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg
 515 520 525
 Pro Gly Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val
 530 535 540
 Arg Val Ser Ala Val Leu Thr Asn Gly Gln Tyr Met Leu Asn Leu Asp
 545 550 555 560
 Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Leu Arg Glu Ala Met Cys
 565 570 575
 Phe Leu Met Asp Pro Asn Leu Gly Arg Ser Val Cys Tyr Val Gln Phe
 580 585 590
 Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp Arg Tyr Ala Asn Arg
 595 600 605
 Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly Leu Asp Gly Ile Gln
 610 615 620
 Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe Asn Arg Thr Ala Leu
 625 630 635 640
 Tyr Gly Tyr Glu Pro Pro Ile Lys Gln Lys Lys Gly Gly Phe Leu Ser
 645 650 655
 Ser Leu Cys Gly Gly Arg Lys Lys Ala Ser Lys Ser Lys Lys Gly Ser
 660 665 670
 Asp Lys Lys Lys Ser Gln Lys His Val Asp Ser Ser Val Pro Val Phe
 675 680 685
 Asn Leu Glu Asp Ile Glu Glu Gly Val Glu Gly Ala Gly Phe Asp Asp
 690 695 700
 Glu Lys Ser Leu Leu Met Ser Gln Met Ser Leu Glu Lys Arg Phe Gly
 705 710 715 720
 Gln Ser Ala Ala Phe Val Ala Ser Thr Leu Met Glu Tyr Gly Gly Val
 725 730 735
 Pro Gln Ser Ala Thr Pro Glu Ser Leu Leu Lys Glu Ala Ile His Val
 740 745 750
 Ile Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Thr Glu Ile Gly
 755 760 765
 Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met
 770 775 780
 His Ala Arg Gly Trp Arg Ser Ile Tyr Cys Met Pro Lys Arg Pro Ala
 785 790 795 800
 Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val
 805 810 815
 Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu Phe Ser Arg His Cys
 820 825 830
 Pro Leu Trp Tyr Gly Tyr Gly Gly Arg Leu Lys Phe Leu Glu Arg Phe
 835 840 845
 Ala Tyr Ile Asn Thr Thr Ile Tyr Pro Leu Thr Ser Ile Pro Leu Leu
 850 855 860
 Ile Tyr Cys Ile Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile
 865 870 875 880

- 16 -

[illegible]

```
<210> 7
<211> 25
<212> DNA
<213> Zea mays
```

<400> 7

atggagggcg acgcggacgg cgtga
25

<210> 8
<211> 25
<212> DNA
<213> Zea mays

<400> 8

ctagcagttg atgccacacg tctgg
25

```
<210> 9
<211> 3780
<212> DNA
<213> Zea mays
```

```
<220>
<221> CDS
<222> (201)...(3423)
```

<400> 9

gtcgacccac gcgctccgag cagcagaagc actgcgcggc attgcagcga tcgagcggga 60
 ggaatttggg gcatggtggt cgccaacgcc gctcggatct agaggccgc acgggccgat 120
 tgggtctccgc ccgcctcgtc ggtgttggtg tcgttggcgt gtggagccgt ctcggtggga 180

- 17 -

gcagcgggga gggagcggag atg gcg gcc aac aag ggg atg gtg gcg ggc tcg 233
Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser
1 5 10

cac aac cgc aac gag ttc gtc atg atc cgc cac gac ggc gat gtg ccg 281
His Asn Arg Asn Glu Phe Val Met Ile Arg His Asp Gly Asp Val Pro
15 20 25

ggc tcg gct aag ccc aca aag agt gcg aat gga cag gtc tgc cag att 329
Gly Ser Ala Lys Pro Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile
30 35 40

tgc ggt gac tct gtg ggt gtt tca gcc act ggt gat gtc ttt gtt gcc 377
Cys Gly Asp Ser Val Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala
45 50 55

tgc aat gag tgt gcc ttc cct gtc tgc cgc cca tgc tat gag tat gag 425
Cys Asn Glu Cys Ala Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu
60 65 70 75

cgc aag gag ggg aac caa tgc tgc ccc cag tgc aag act aga tac aag 473
Arg Lys Glu Gly Asn Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys
80 85 90

aga cag aaa ggt agc cct cga gtt cat ggt gat gag gat gag gaa gat 521
Arg Gln Lys Gly Ser Pro Arg Val His Gly Asp Glu Asp Glu Glu Asp
95 100 105

gtt gat gac cta gac aat gaa ttc aac tac aag caa ggc agt ggg aaa 569
Val Asp Asp Leu Asp Asn Glu Phe Asn Tyr Lys Gln Gly Ser Gly Lys
110 115 120

ggc cca gag tgg caa ctg caa gga gat gat gct gat ctg tct tca tct 617
Gly Pro Glu Trp Gln Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser
125 130 135

gct cgc cat gag cca cat cat cgg att cca cgc ctg aca agc ggt caa 665
Ala Arg His Glu Pro His His Arg Ile Pro Arg Leu Thr Ser Gly Gln
140 145 150 155

cag ata tct gga gag att cct gat gct tcc cct gac cgt cat tct atc 713
Gln Ile Ser Gly Glu Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile
160 165 170

cgc agt cca aca tcg agc tat gtt gat cca agc gtc cca gtt cct gtg 761
Arg Ser Pro Thr Ser Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val
175 180 185

agg att gtg gac ccc tcg aag gac ttg aat tcc tat ggg ctt aat agt 809
Arg Ile Val Asp Pro Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser
190 195 200

gtt gac tgg aag gaa aga gtt gag agc tgg agg gtt aaa cag gac aaa 857
Val Asp Trp Lys Glu Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys
205 210 215

aat atg atg caa gtg act aat aaa tat cca gag gct aga gga gga gac 905
Asn Met Met Gln Val Thr Asn Lys Tyr Pro Glu Ala Arg Gly Gly Asp

- 18 -

220	225	230	235	
atg gag ggg act ggc tca aat gga gaa nat atg caa atg gtt gat gat				953
Met Glu Gly Thr Gly Ser Asn Gly Glu Xaa Met Gln Met Val Asp Asp	240	245	250	
gca cgg cta cct ttg agc cgt atc gtg cca att tcc tca aac cag ctc				1001
Ala Arg Leu Pro Leu Ser Arg Ile Val Pro Ile Ser Ser Asn Gln Leu	255	260	265	
aac ctt tac cgg gta gtg atc att ctc cgt ctt atc atc ctg tgc ttc				1049
Asn Leu Tyr Arg Val Val Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe	270	275	280	
ttc ttc cag tat cgt gtc agt cat cca gtg cgt gat gct tat gga tta				1097
Phe Phe Gln Tyr Arg Val Ser His Pro Val Arg Asp Ala Tyr Gly Leu	285	290	295	
tgg cta gta tct gtt atc tgc gag gtc tgg ttt gcc ttg tct tgg ctt				1145
Trp Leu Val Ser Val Ile Cys Glu Val Trp Phe Ala Leu Ser Trp Leu	300	305	310	315
cta gat cag ttc cca aaa tgg tat cca atc aac cgt gag aca tat ctt				1193
Leu Asp Gln Phe Pro Lys Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu	320	325	330	
gac agg ctt gca ttg agg tat gat aga gag gga gag cca tca cag ctg				1241
Asp Arg Leu Ala Leu Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu	335	340	345	
gct ccc att gat gtc ttc gtc agt aca gtg gat cca ttg aag gaa cct				1289
Ala Pro Ile Asp Val Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro	350	355	360	
cca ctg atc aca gcc aac act gtt ttg tcc att ctt tct gtg gat tac				1337
Pro Leu Ile Thr Ala Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr	365	370	375	
cct gtt gac aaa gtg tca tgc tat gtt tct gat gat ggt tca gct atg				1385
Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ser Ala Met	380	385	390	395
ctg act ttt gag tct ctc tca gaa acc gca gaa ttt gct aga aag tgg				1433
Leu Thr Phe Glu Ser Leu Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp	400	405	410	
gtt ccc ttt tgt aag aag cac aat att gaa cca aga gct cca gaa ttt				1481
Val Pro Phe Cys Lys Lys His Asn Ile Glu Pro Arg Ala Pro Glu Phe	415	420	425	
tac ttt gct caa aaa ata gat tac ctg aag gac aaa att caa cct tca				1529
Tyr Phe Ala Gln Lys Ile Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser	430	435	440	
ttt gtt aag gaa aga cgc gca atg aag agg gag tat gaa gaa ttc aaa				1577
Phe Val Lys Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys	445	450	455	

- 19 -

gta aga atc aat gcc ctt gtt gcc aaa gca cag aaa gtg cct gaa gag	1625
Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu	
460 465 470 475	
ggg tgg acc atg gct gat gga act gca tgg cct ggg aat aat cct agg	1673
Gly Trp Thr Met Ala Asp Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg	
480 485 490	
gac cat cct ggc atg att cag gtt ttc ttg ggg cac agt ggt ggg ctc	1721
Asp His Pro Gly Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu	
495 500 505	
gac act gat gga aat gag tta cca cgt ctt gtc tat gtc tct cgt gaa	1769
Asp Thr Asp Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu	
510 515 520	
aag aga cca ggc ttt cag cat cac aag aag gct ggt gca atg aat gcg	1817
Lys Arg Pro Gly Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala	
525 530 535	
ctg att cgt gta tct gct gtg ctg aca aat ggt gcc tat ctt ctc aat	1865
Leu Ile Arg Val Ser Ala Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn	
540 545 550 555	
gtg gat tgc gac cat tac ttc aat agc agc aaa gct ctt aga gaa gca	1913
Val Asp Cys Asp His Tyr Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala	
560 565 570	
atg tgc ttc atg atg gat ccg gct cta gga agg aaa act tgt tat gta	1961
Met Cys Phe Met Met Asp Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val	
575 580 585	
caa ttt cca cag aga ttt gat ggc att gac ttg cac gat cga tat gct	2009
Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Leu His Asp Arg Tyr Ala	
590 595 600	
aat cgg aac ata gtt ttc ttt gat atc aac atg aaa ggt ctg gat ggc	2057
Asn Arg Asn Ile Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly	
605 610 615	
att cag ggt cca gtt tac gtg gga aca gga tgc tgt ttc aat aga cag	2105
Ile Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Cys Phe Asn Arg Gln	
620 625 630 635	
gct ttg tat gga tac gat cct gtt ttg act gaa gct gat ctg gag cca	2153
Ala Leu Tyr Gly Tyr Asp Pro Val Leu Thr Glu Ala Asp Leu Glu Pro	
640 645 650	
aac att gtt att aag agc tgc tgt ggt aga agg aag aaa aag aac aag	2201
Asn Ile Val Ile Lys Ser Cys Cys Gly Arg Arg Lys Lys Lys Asn Lys	
655 660 665	
agt tat atg gat agt caa agc cgt att atg aag aga aca gaa tct tca	2249
Ser Tyr Met Asp Ser Gln Ser Arg Ile Met Lys Arg Thr Glu Ser Ser	
670 675 680	
gct ccc atc ttc aat atg gaa gac atc gaa gag ggt att gaa ggt tac	2297
Ala Pro Ile Phe Asn Met Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr	

- 20 -

685	690	695	
gag gat gaa agg tca gtg ctt atg tcc cag agg aaa ttg gag aaa cgc Glu Asp Glu Arg Ser Val Leu Met Ser Gln Arg Lys Leu Glu Lys Arg 700 705 710 715			2345
ttt ggt cag tct cct att ttc att gca tcc acc ttt atg aca caa ggt Phe Gly Gln Ser Pro Ile Phe Ile Ala Ser Thr Phe Met Thr Gln Gly 720 725 730			2393
ggc ata cca cct tca aca aac cca gct tct cta cta aag gaa gct atc Gly Ile Pro Pro Ser Thr Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile 735 740 745			2441
cat gtc atc agt tgt gga tat gag gac aaa act gaa tgg gga aaa gag His Val Ile Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu 750 755 760			2489
att ggc tgg atc tat ggt tca gta acg gag gat att ctg act ggg ttt Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe 765 770 775			2537
aaa atg cat gca agg ggc tgg caa tca atc tac tgc atg cca cca cga Lys Met His Ala Arg Gly Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg 780 785 790 795			2585
cct tgt ttc aag ggt tct gca cca atc aat ctt tcc gat cgt ctt aat Pro Cys Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn 800 805 810			2633
cag gtg ctc cgt tgg gct ctt ggg tca gtg gaa att ctg ctt agt aga Gln Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu Leu Ser Arg 815 820 825			2681
cat tgt cct atc tgg tat ggt tac aat gga cga ttg aag ctt ttg gag His Cys Pro Ile Trp Tyr Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu 830 835 840			2729
agg ctg gct tac atc aac act att gta tat cca atc aca tcc att ccg Arg Leu Ala Tyr Ile Asn Thr Ile Val Tyr Pro Ile Thr Ser Ile Pro 845 850 855			2777
ctt att gcc tat tgt gtg ctt ccc gct atc tgc ctc ctt acc aat aaa Leu Ile Ala Tyr Cys Val Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys 860 865 870 875			2825
ttt atc att cct gag att agc aat tat gct ggg atg ttc ttc att ctt Phe Ile Ile Pro Glu Ile Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu 880 885 890			2873
ctt ttc gcc tcc att ttt gcc act ggt ata ttg gag ctt aga tgg agt Leu Phe Ala Ser Ile Phe Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser 895 900 905			2921
ggt gtt ggc att gaa gat tgg tgg aga aat gag cag ttt tgg gtt att Gly Val Gly Ile Glu Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile 910 915 920			2969

- 21 -

ggt ggc acc tct gcc cat ctc ttc gca gtg ttc cag ggt ctg ctg aaa 3017
 Gly Gly Thr Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys
 925 930 935

gtg ttg gct ggg att gat acc aac ttc aca gtt acc tca aag gca tct 3065
 Val Leu Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser
 940 945 950 955

gat gag gat ggc gac ttt gct gag cta tat gtg ttc aag tgg acc agt 3113
 Asp Glu Asp Gly Asp Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser
 960 965 970

ttg ctc att cct ccg acc act gtt ctt gtc att aac ctg gtc gga atg 3161
 Leu Leu Ile Pro Pro Thr Thr Val Leu Val Ile Asn Leu Val Gly Met
 975 980 985

gtg gca gga att tct tat gcc att aac agt ggc tac caa tcc tgg ggt 3209
 Val Ala Gly Ile Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly
 990 995 1000

ccg ctc ttt gga aag ctg ttc ttc tcg atc tgg gtg atc ctc cat ctc 3257
 Pro Leu Phe Gly Lys Leu Phe Phe Ser Ile Trp Val Ile Leu His Leu
 1005 1010 1015

tac ccc ttc ctc aag ggt ctc atg gga agg cag aac cgc aca cca aca 3305
 Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr
 1020 1025 1030 1035

atc gtc att gtc tgg tcc atc ctt ctt gca tct atc ttc tcc ttg ctg 3353
 Ile Val Ile Val Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu
 1040 1045 1050

tgg gtg aag atc gat cct ttc atc tcc ccg aca cag aaa gct gct gcc 3401
 Trp Val Lys Ile Asp Pro Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala
 1055 1060 1065

ttg ggg caa tgt ggc gtc aac t gctgacgag acagtgactc ttatttgaag 3453
 Leu Gly Gln Cys Gly Val Asn
 1070

aggctcaatc aagatctgcc cctcgtgta aatacctgag gaggetagat gggaattcct 3513
 tttgtttag gtgaggatgg atttgcattc aagttatgcc tctgttcatt agcttcttcc 3573
 gtgccggtgc tgctgcggac taagaatcac ggagccttcc taccttccat gtagcgccag 3633
 ccagcagcgt aagatgtgaa ttttgaagtt ttgttatgcg tgcagtttat tgttttagag 3693
 taaattatca tttgtttgtg ggaactgttc acacgagctt ataatggcaa tgctgttatt 3753
 taaaaaaaa aaaaaaaggg cggccgc 3780

<210> 10
 <211> 1075
 <212> PRT
 <213> Zea mays

<400> 10
 Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 Phe Val Met Ile Arg His Asp Gly Asp Val Pro Gly Ser Ala Lys Pro
 20 25 30
 Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Ser Val

[illegible]

- 23 -

500	505	510
Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe		
515	520	525
Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser		
530	535	540
Ala Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His		
545	550	555
Tyr Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met		
565	570	575
Asp Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg		
580	585	590
Phe Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val		
595	600	605
Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val		
610	615	620
Tyr Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr		
625	630	635
Asp Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Ile Lys		
645	650	655
Ser Cys Cys Gly Arg Arg Lys Lys Lys Asn Lys Ser Tyr Met Asp Ser		
660	665	670
Gln Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe Asn		
675	680	685
Met Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg Ser		
690	695	700
Val Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser Pro		
705	710	715
Ile Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro Ser		
725	730	735
Thr Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys		
740	745	750
Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr		
755	760	765
Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg		
770	775	780
Gly Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly		
785	790	795
Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp		
805	810	815
Ala Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile Trp		
820	825	830
Tyr Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr Ile		
835	840	845
Asn Thr Ile Val Tyr Pro Ile Thr Ser Ile Pro Leu Ile Ala Tyr Cys		
850	855	860
Val Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu		
865	870	875
Ile Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser Ile		
885	890	895
Phe Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu		
900	905	910
Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala		
915	920	925
His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile		
930	935	940
Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp		
945	950	955
Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro		
	960	

- 24 -

965 970 975
 Thr Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser
 980 985 990
 Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys
 995 1000 1005
 Leu Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys
 1010 1015 1020
 Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp
 1025 1030 1035 1040
 Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp
 1045 1050 1055
 Pro Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys Gly
 1060 1065 1070
 Val Asn Cys
 1075

<210> 11
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 11
 atggcgccca acaaggggat ggtgg
 25

<210> 12
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 12
 tcagcagttg acgccacatt gcccc
 25

<210> 13
 <211> 3725
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (179)...(3398)

<400> 13
 gcagcagcag caccaccact gcgcggcatt gcagcgagca agcgggaggg atctggggca 60
 tgggtggcggc cgctgccgct gccgctcgga tctagagggc cgcacgggct gattgccctc 120
 cgccggcctc gtcggtgtcg gtggagtgtg aatcggtgtg tgtaggagga gcgcggag 178
 atg gcg gcc aac aag ggg atg gtg gca ggc tct cac aac cgc aac gag 226
 Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 ttc gtc atg atc cgc cac gac ggc gac gcg cct gtc ccg gct aag ccc 274
 Phe Val Met Ile Arg His Asp Gly Asp Ala Pro Val Pro Ala Lys Pro
 20 25 30
 acg aag agt gcg aat ggg cag gtc tgc cag att tgt ggc gac act gtt 322
 Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Thr Val
 35 40 45

- 25 -

ggc gtt tca gcc act ggt gat gtc ttt gtt gcc tgc aat gag tgt gcc Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys Ala 50 55 60	370
ttc cct gtc tgc cgc cct tgc tat gag tac gag cgc aag gaa ggg aac Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly Asn 65 70 75 80	418
caa tgc tgc cct cag tgc aag act aga tac aag aga cag aaa ggt agc Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser 85 90 95	466
cct cga gtt cat ggt gat gat gag gag gaa gat gtt gat gac ctg gac Pro Arg Val His Gly Asp Asp Glu Glu Glu Asp Val Asp Asp Leu Asp 100 105 110	514
aat gaa ttc aac tat aag caa ggc aat ggg aag ggc cca gag tgg cag Asn Glu Phe Asn Tyr Lys Gln Gly Asn Gly Lys Gly Pro Glu Trp Gln 115 120 125	562
ctt caa gga gat gac gct gat ctg tct tca tct gct cgc cat gac cca Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Asp Pro 130 135 140	610
cac cat cgg att cca cgc ctt aca agt gga caa cag ata tct gga gag His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly Glu 145 150 155 160	658
atc cct gat gca tcc cct gac cgt cat tct atc cgc agt cca aca tcg Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr Ser 165 170 175	706
agc tat gtt gat cca agc gtt cca gtt cct gtg agg att gtg gac ccc Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp Pro 180 185 190	754
tcg aag gac ttg aat tcc tat ggg ctt aat agt gtt gac tgg aag gaa Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys Glu 195 200 205	802
aga gtt gag agc tgg agg gtt aaa cag gac aaa aat atg ttg caa gtg Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Leu Gln Val 210 215 220	850
act aat aaa tat cca gag gct aga gga gac atg gag ggg act ggc tca Thr Asn Lys Tyr Pro Glu Ala Arg Gly Asp Met Glu Gly Thr Gly Ser 225 230 235 240	898
aat gga gaa gat atg caa atg gtt gat gat gca cgc cta cct ttg agc Asn Gly Glu Asp Met Gln Met Val Asp Asp Ala Arg Leu Pro Leu Ser 245 250 255	946
cgc att gtg cca att tcc tca aac cag ctc aac ctt tac cgg ata gta Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg Ile Val 260 265 270	994
atc att ctc cgt ctt atc atc ctg tgc ttc ttc ttc caa tat cgt atc	1042

- 26 -

Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr Arg Ile	
275 280 285	
agt cat cca gtg cgt aat gct tat gga ttg tgg cta gta tct gtt atc	1090
Ser His Pro Val Arg Asn Ala Tyr Gly Leu Trp Leu Val Ser Val Ile	
290 295 300	
tgt gag gtc tgg ttt gcc ttg tcc tgg ctt cta gat cag ttc cca aaa	1138
Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe Pro Lys	
305 310 315 320	
tgg tat cca atc aac cgt gag aca tat ctc gac agg ctt gca ttg agg	1186
Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu Arg	
325 330 335	
tat gat aga gag gga gag cca tca cag ctg gct ccc att gat gtc ttt	1234
Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp Val Phe	
340 345 350	
gtc agt aca gtg gat cca ttg aag gaa cct cca ctg atc aca gcc aac	1282
Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala Asn	
355 360 365	
act gtt ttg tcc att ctt gct gtg gat tac cct gtt gac aaa gtg tca	1330
Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser	
370 375 380	
tgc tat gtt tct gat gat ggc tca gct atg ctg act ttt gag tct ctc	1378
Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser Leu	
385 390 395 400	
tct gaa act gcc gaa ttt gct aga aag tgg gtt ccc ttt tgt aag aag	1426
Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys	
405 410 415	
cac aat att gaa cca aga gct cca gaa ttt tac ttt gct caa aaa ata	1474
His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln Lys Ile	
420 425 430	
gat tac ctg aag gac aaa att caa cct tca ttt gtt aag gaa aga cga	1522
Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg Arg	
435 440 445	
gca atg aag aga gag tat gaa gaa ttc aaa ata aga atc aat gcc ctt	1570
Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile Arg Ile Asn Ala Leu	
450 455 460	
gtt gcc aaa gca cag aaa gtg cct gaa gag ggg tgg acc atg gct gat	1618
Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Ala Asp	
465 470 475 480	
gga act gct tgg cct ggg aat aac cct agg gac cat cct ggc atg att	1666
Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile	
485 490 495	
cag gtg ttc ttg ggg cac agt ggt ggg ctt gac act gat gga aat gaa	1714
Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn Glu	
500 505 510	

- 27 -

tta cca cgt ctt gtc tat gtc tct cgt gaa aag aga cca ggc ttt cag	1762
Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln	
515 520 525	
cat cac aag aag gct ggt gca atg aat gca ctg att cgt gta tct gct	1810
His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala	
530 535 540	
gtg ctg aca aat ggt gcc tat ctt ctc aat gtg gat tgt gac cat tac	1858
Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His Tyr	
545 550 555 560	
ttc aat agc agc aaa gct ctt aga gaa gca atg tgc ttc atg atg gat	1906
Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met Asp	
565 570 575	
cca gct cta gga agg aaa act tgt tat gta caa ttt cca caa aga ttt	1954
Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg Phe	
580 585 590	
gat ggc att gac ttg cac gat cga tat gct aat agg aac ata gtc ttc	2002
Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val Phe	
595 600 605	
ttt gat atc aac atg aaa ggt cta gat ggc att cag ggt cca gtc tat	2050
Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr	
610 615 620	
gtg gga aca gga tgc tgt ttc aat agg cag gct ttg tat gga tat gat	2098
Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr Asp	
625 630 635 640	
cct gtt ttg act gaa gct gat ctg gaa cct aac att gtt gtt aag agc	2146
Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Val Lys Ser	
645 650 655	
tgc tgt ggt aga agg aag aga aag aac aag agt tat atg gat agt caa	2194
Cys Cys Gly Arg Arg Lys Arg Lys Asn Lys Ser Tyr Met Asp Ser Gln	
660 665 670	
agc cgt att atg aag aga aca gaa tct tca gct ccc atc ttt aac atg	2242
Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe Asn Met	
675 680 685	
gaa gac atc gag gag ggt att gaa ggt tat gag gat gaa agg tca gtg	2290
Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg Ser Val	
690 695 700	
ctt atg tcc cag agg aaa ttg gag aaa cgc ttt ggt cag tct cca atc	2338
Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser Pro Ile	
705 710 715 720	
ttc att gca tcc acc ttt atg act caa ggt ggc ata cca cct tca aca	2386
Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro Ser Thr	
725 730 735	
aac cca gct tct cta ctg aag gaa gct atc cat gtt atc agc tgt ggg	2434

- 28 -

Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly	
740 745 750	
tac gag gac aaa act gaa tgg gga aaa gag att ggc tgg atc tat ggt	2482
Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly	
755 760 765	
tca gtt aca gag gat att ctg act ggg ttt aaa atg cat gca aga ggc	2530
Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly	
770 775 780	
tgg caa tca atc tac tgc atg cca cca cga cct tgt ttc aag ggt tct	2578
Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser	
785 790 795 800	
gca cca atc aat ctt tct gat cgt ctt aat cag gtg ctc cgt tgg gct	2626
Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala	
805 810 815	
ctt ggg tca gtg gaa att ctg ctt agc aga cat tgt cct ata tgg tat	2674
Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile Trp Tyr	
820 825 830	
ggc tac aat ggg cga ttg aag ctt ttg gag agg ctg gct tac att aac	2722
Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr Ile Asn	
835 840 845	
acc att gtt tat cca atc aca tct gtt ccg ctt atc gcc tat tgt gtg	2770
Thr Ile Val Tyr Pro Ile Thr Ser Val Pro Leu Ile Ala Tyr Cys Val	
850 855 860	
ctt cct gct atc tgt ctt ctt acc aat aaa ttt atc att cct gag att	2818
Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile	
865 870 875 880	
agt aat tat gct gga atg ttc ttc att ctt ctt ttt gcc tcc att ttc	2866
Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser Ile Phe	
885 890 895	
gca act ggt ata ttg gag ctc aga tgg agt ggt gtt ggc att gaa gat	2914
Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp	
900 905 910	
tgg tgg aga aat gag cag ttt tgg gtt att ggt ggc acc tct gcc cat	2962
Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His	
915 920 925	
ctc ttc gcg gtg ttc cag ggt ctg ctg aaa gtg ttg gct ggg att gat	3010
Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp	
930 935 940	
acc aac ttc aca gtt acc tca aag gca tct gat gag gat ggc gac ttt	3058
Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp Phe	
945 950 955 960	
gct gag cta tat gtg ttc aag tgg acc agt ttg ctc atc cct ccg acc	3106
Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr	
965 970 975	

- 29 -

act gtt ctt gtc att aac ctg gtc gga atg gtg gca gga att tcg tat 3154
 Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr
 980 985 990

gcc att aac agc ggc tac caa tcc tgg ggt ccg ctc ttt gga aag ctg 3202
 Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu
 995 1000 1005

ttc ttc tcg atc tgg gtg atc ctc cat ctc tac ccc ttc ctc aag ggt 3250
 Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly
 1010 1015 1020

ctc atg ggc agg cag aac cgc acg cca aca atc gtc atc gtt tgg tcc 3298
 Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser
 1025 1030 1035 1040

atc ctc ctt gcg tct atc ttc tcc ttg ctg tgg gtg aag atc gat cct 3346
 Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro
 1045 1050 1055

ttc atc tcc ccg aca cag aaa gct gcc gcc ttg ggg caa tgt ggt gtg 3394
 Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys Gly Val
 1060 1065 1070

aac t gctgatccag attgtgactc ttatctgaag aggctcagcc aaagatctgc 3448
 Asn

cccctcgtgt aaatacctga gggggctaga tgggaatttt ttgttgtaga tgaggatgga 3508
 tctgcaccca agttatgcct ctgtttatta gcttcttcgg tgccgggtgct gctgcagaca 3568
 atcatggagc ctttctacct tgcctgtagt gctggccagc agcgtaaatt gtgaattctg 3628
 cattttttta tacgtggtgt ttattgtttt agagtaaatt atcatttgtt tgaggtaact 3688
 attcacacga actatatggc aatgctgtta tttaaaa 3725

<210> 14
 <211> 1074
 <212> PRT
 <213> Zea mays

<400> 14
 Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 Phe Val Met Ile Arg His Asp Gly Asp Ala Pro Val Pro Ala Lys Pro
 20 25 30
 Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Thr Val
 35 40 45
 Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys Ala
 50 55 60
 Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly Asn
 65 70 75 80
 Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser
 85 90 95
 Pro Arg Val His Gly Asp Asp Glu Glu Glu Asp Val Asp Asp Leu Asp
 100 105 110
 Asn Glu Phe Asn Tyr Lys Gln Gly Asn Gly Lys Gly Pro Glu Trp Gln
 115 120 125
 Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Asp Pro

- 30 -

130	135	140
His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly Glu		
145	150	155
Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr Ser		160
	165	170
Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp Pro		175
	180	185
Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys Glu		190
	195	200
Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Leu Gln Val		205
	210	215
Thr Asn Lys Tyr Pro Glu Ala Arg Gly Asp Met Glu Gly Thr Gly Ser		220
225	230	235
Asn Gly Glu Asp Met Gln Met Val Asp Asp Ala Arg Leu Pro Leu Ser		240
	245	250
Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg Ile Val		255
	260	265
Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr Arg Ile		270
	275	280
Ser His Pro Val Arg Asn Ala Tyr Gly Leu Trp Leu Val Ser Val Ile		285
	290	295
Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe Pro Lys		300
305	310	315
Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu Arg		320
	325	330
Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp Val Phe		335
	340	345
Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala Asn		350
	355	360
Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser		365
	370	375
Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser Leu		380
385	390	395
Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys		400
	405	410
His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln Lys Ile		415
	420	425
Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg Arg		430
	435	440
Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile Arg Ile Asn Ala Leu		445
	450	455
Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Ala Asp		460
465	470	475
Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile		480
	485	490
Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn Glu		495
	500	505
Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln		510
	515	520
His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala		525
	530	535
Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His Tyr		540
545	550	555
Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met Asp		560
	565	570
Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg Phe		575
	580	585
Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val Phe		590

- 31 -

595	600	605
Phe Asp Ile Asn Met Lys Gly	Leu Asp Gly Ile Gln Gly	Pro Val Tyr
610	615	620
Val Gly Thr Gly Cys Cys Phe	Asn Arg Gln Ala Leu Tyr	Gly Tyr Asp
625	630	635
Pro Val Leu Thr Glu Ala Asp	Leu Glu Pro Asn Ile Val	Val Lys Ser
645	650	655
Cys Cys Gly Arg Arg Lys Arg	Lys Asn Lys Ser Tyr Met	Asp Ser Gln
660	665	670
Ser Arg Ile Met Lys Arg Thr	Glu Ser Ser Ala Pro Ile	Phe Asn Met
675	680	685
Glu Asp Ile Glu Glu Gly Ile	Glu Gly Tyr Glu Asp Glu	Arg Ser Val
690	695	700
Leu Met Ser Gln Arg Lys Leu	Glu Lys Arg Phe Gly Gln	Ser Pro Ile
705	710	715
Phe Ile Ala Ser Thr Phe Met	Thr Gln Gly Gly Ile Pro	Pro Ser Thr
725	730	735
Asn Pro Ala Ser Leu Leu Lys	Glu Ala Ile His Val Ile	Ser Cys Gly
740	745	750
Tyr Glu Asp Lys Thr Glu Trp	Gly Lys Glu Ile Gly Trp	Ile Tyr Gly
755	760	765
Ser Val Thr Glu Asp Ile Leu	Thr Gly Phe Lys Met His	Ala Arg Gly
770	775	780
Trp Gln Ser Ile Tyr Cys Met	Pro Pro Arg Pro Cys Phe	Lys Gly Ser
785	790	795
Ala Pro Ile Asn Leu Ser Asp	Arg Leu Asn Gln Val Leu	Arg Trp Ala
805	810	815
Leu Gly Ser Val Glu Ile Leu	Leu Ser Arg His Cys Pro	Ile Trp Tyr
820	825	830
Gly Tyr Asn Gly Arg Leu Lys	Leu Leu Glu Arg Leu Ala	Tyr Ile Asn
835	840	845
Thr Ile Val Tyr Pro Ile Thr	Ser Val Pro Leu Ile Ala	Tyr Cys Val
850	855	860
Leu Pro Ala Ile Cys Leu Leu	Thr Asn Lys Phe Ile Ile	Pro Glu Ile
865	870	875
Ser Asn Tyr Ala Gly Met Phe	Phe Ile Leu Leu Phe Ala	Ser Ile Phe
885	890	895
Ala Thr Gly Ile Leu Glu Leu	Arg Trp Ser Gly Val Gly	Ile Glu Asp
900	905	910
Trp Trp Arg Asn Glu Gln Phe	Trp Val Ile Gly Gly Thr	Ser Ala His
915	920	925
Leu Phe Ala Val Phe Gln Gly	Leu Leu Lys Val Leu Ala	Gly Ile Asp
930	935	940
Thr Asn Phe Thr Val Thr Ser	Lys Ala Ser Asp Glu Asp	Gly Asp Phe
945	950	955
Ala Glu Leu Tyr Val Phe Lys	Trp Thr Ser Leu Leu Ile	Pro Pro Thr
965	970	975
Thr Val Leu Val Ile Asn Leu	Val Gly Met Val Ala Gly	Ile Ser Tyr
980	985	990
Ala Ile Asn Ser Gly Tyr Gln	Ser Trp Gly Pro Leu Phe	Gly Lys Leu
995	1000	1005
Phe Phe Ser Ile Trp Val Ile	Leu His Leu Tyr Pro Phe	Leu Lys Gly
1010	1015	1020
Leu Met Gly Arg Gln Asn Arg	Thr Pro Thr Ile Val Ile	Val Trp Ser
1025	1030	1035
Ile Leu Leu Ala Ser Ile Phe	Ser Leu Leu Trp Val Lys	Ile Asp Pro
1045	1050	1055
Phe Ile Ser Pro Thr Gln Lys	Ala Ala Ala Leu Gly	Gln Cys Gly Val

- 32 -

1060
Asn Cys

1065

1070

<210> 15
<211> 25
<212> DNA
<213> Zea mays

<400> 15
atggcgccca acaaggggat ggtgg
25

<210> 16
<211> 25
<212> DNA
<213> Zea mays

<400> 16
tcagcagttc acaccacatt gcccc
25

<210> 17
<211> 3969
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (144)... (3399)

<400> 17
cttctccctc gtcggtgcgg cgtggcgcg ctcggcggttc ggtgagaaac cactcggggg 60
atgaggatct gctgctagag tgagaggagc tacggtcagt atcctctgcc ttgctcgggc 120
gcggaagtgg aggggaggaa gcg atg gag gcg agc gcc ggg ctg gtg gcc ggc 173
Met Glu Ala Ser Ala Gly Leu Val Ala Gly
1 5 10

tcc cac aac cgc aac gag ctc gtc gtc atc cgc cgc gac ggc gat ccc 221
Ser His Asn Arg Asn Glu Leu Val Val Ile Arg Arg Asp Gly Asp Pro
15 20 25

ggg ccg aag ccg ccg cgg gag cag aac ggg cag gtg tgc cag att tgc 269
Gly Pro Lys Pro Pro Arg Glu Gln Asn Gly Gln Val Cys Gln Ile Cys
30 35 40

ggc gac gac gtc ggc ctt gcc ccc ggc ggg gac ccc ttc gtg gcg tgc 317
Gly Asp Asp Val Gly Leu Ala Pro Gly Gly Asp Pro Phe Val Ala Cys
45 50 55

aac gag tgc gcc ttc ccc gtc tgc cgg gac tgc tac gaa tac gag cgc 365
Asn Glu Cys Ala Phe Pro Val Cys Arg Asp Cys Tyr Glu Tyr Glu Arg
60 65 70

cgg gag ggc acg cag aac tgc ccc cag tgc aag act cga tac aag cgc 413
Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg
75 80 85 90

- 33 -

ctc aag ggc tgc caa cgt gtg acc ggt gac gag gag gag gac ggc gtc	461
Leu Lys Gly Cys Gln Arg Val Thr Gly Asp Glu Glu Glu Asp Gly Val	
95 100 105	
gat gac ctg gac aac gag ttc aac tgg gac ggc cat gac tcg cag tct	509
Asp Asp Leu Asp Asn Glu Phe Asn Trp Asp Gly His Asp Ser Gln Ser	
110 115 120	
gtg gcc gag tcc atg ctc tac ggc cac atg agc tac ggc cgt gga ggt	557
Val Ala Glu Ser Met Leu Tyr Gly His Met Ser Tyr Gly Arg Gly Gly	
125 130 135	
gac cct aat ggc gcg cca caa gct ttc cag ctc aac ccc aat gtt cca	605
Asp Pro Asn Gly Ala Pro Gln Ala Phe Gln Leu Asn Pro Asn Val Pro	
140 145 150	
ctc ctc acc aac ggg caa atg gtg gat gac atc cca ccg gag cag cac	653
Leu Leu Thr Asn Gly Gln Met Val Asp Asp Ile Pro Pro Glu Gln His	
155 160 165 170	
gcg ctg gtg cct tct ttc atg ggt ggt ggg gga aag agg ata cat ccc	701
Ala Leu Val Pro Ser Phe Met Gly Gly Gly Lys Arg Ile His Pro	
175 180 185	
ctt cct tat gcg gat ccc agc tta cct gtg caa ccc agg tct atg gac	749
Leu Pro Tyr Ala Asp Pro Ser Leu Pro Val Gln Pro Arg Ser Met Asp	
190 195 200	
cca tcc aag gat ctt gct gca tat ggg tat ggt agt gtt gct tgg aag	797
Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr Gly Ser Val Ala Trp Lys	
205 210 215	
gaa cgg atg gag aat tgg aag cag aga caa gag agg atg cac cag acg	845
Glu Arg Met Glu Asn Trp Lys Gln Arg Gln Glu Arg Met His Gln Thr	
220 225 230	
ggg aat gat ggt ggt ggt gat gat ggt gac gat gct gat cta cca cta	893
Gly Asn Asp Gly Gly Gly Asp Asp Gly Asp Asp Ala Asp Leu Pro Leu	
235 240 245 250	
atg gat gaa gca aga caa caa ctg tcc agg aaa att cca ctt cca tca	941
Met Asp Glu Ala Arg Gln Gln Leu Ser Arg Lys Ile Pro Leu Pro Ser	
255 260 265	
agc cag att aat cca tat agg atg att atc att att cgg ctt gtg gtt	989
Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile Ile Ile Arg Leu Val Val	
270 275 280	
ttg ggg ttc ttc ttc cac tac cga gtg atg cat ccg gtg aat gat gca	1037
Leu Gly Phe Phe Phe His Tyr Arg Val Met His Pro Val Asn Asp Ala	
285 290 295	
ttt gct ttg tgg ctc ata tct gtt atc tgt gaa atc tgg ttt gcc atg	1085
Phe Ala Leu Trp Leu Ile Ser Val Ile Cys Glu Ile Trp Phe Ala Met	
300 305 310	
tct tgg att ctt gat caa ttc cca aag tgg ttc cct att gag aga gag	1133
Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Phe Pro Ile Glu Arg Glu	

- 34 -

315	320	325	330	
act tac cta gac cgg ctg tca ctg agg ttc gac aag gaa ggc cag cca				1181
Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe Asp Lys Glu Gly Gln Pro	335	340	345	
tct caa ctt gct cca att gat ttc ttt gtc agt acg gtt gat ccc tta				1229
Ser Gln Leu Ala Pro Ile Asp Phe Phe Val Ser Thr Val Asp Pro Leu	350	355	360	
aag gaa cct cct ttg gtc aca aca aat act gtt cta tct atc ctt tcg				1277
Lys Glu Pro Pro Leu Val Thr Thr Asn Thr Val Leu Ser Ile Leu Ser	365	370	375	
gtg gat tat cct gtt gat aag gtt tct tgc tat gtt tct gat gat ggt				1325
Val Asp Tyr Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly	380	385	390	
gct gca atg cta acg ttt gaa gca tta tct gaa aca tct gaa ttt gca				1373
Ala Ala Met Leu Thr Phe Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala	395	400	405	410
aag aaa tgg gtt cct ttc tgc aaa cgg tac aat att gaa cct cgc gct				1421
Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr Asn Ile Glu Pro Arg Ala	415	420	425	
cca gag tgg tac ttc caa cag aag ata gac tac ttg aaa gac aag gtg				1469
Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val	430	435	440	
gca gca aac ttt gtt agg gag agg aga gca atg aag aga gag tat gag				1517
Ala Ala Asn Phe Val Arg Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu	445	450	455	
gaa ttc aag gtg aga atc aat gcc tta gtt gcc aaa gcc cag aaa gtt				1565
Glu Phe Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Val	460	465	470	
cct gaa gaa gga tgg aca atg caa gat gga acc ccc tgg cct gga aac				1613
Pro Glu Glu Gly Trp Thr Met Gln Asp Gly Thr Pro Trp Pro Gly Asn	475	480	485	490
aat gtt cgt gat cat cct gga atg att cag gtc ttc ctt ggc caa agc				1661
Asn Val Arg Asp His Pro Gly Met Ile Gln Val Phe Leu Gly Gln Ser	495	500	505	
gga ggc ctt gac tgt gag gga aat gaa ctg cca cga ttg gtt tat gtt				1709
Gly Gly Leu Asp Cys Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val	510	515	520	
tct aga gag aaa cga cca ggc tat aac cat cat aag aaa gct ggt gct				1757
Ser Arg Glu Lys Arg Pro Gly Tyr Asn His His Lys Lys Ala Gly Ala	525	530	535	
atg aat gca ttg gtc cga gtc tct gct gta cta aca aat gct cca tat				1805
Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Ala Pro Tyr	540	545	550	

- 35 -

ttg tta aac ttg gat tgt gat cac tac atc aac aac agc aag gct ata	1853
Leu Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Ile	
555 560 565 570	
aag gaa gca atg tgt ttt atg atg gac cct tta cta gga aag aag gtt	1901
Lys Glu Ala Met Cys Phe Met Met Asp Pro Leu Leu Gly Lys Lys Val	
575 580 585	
tgc tat gta cag ttc cct caa aga ttt gat ggg att gat cgc cat gac	1949
Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg His Asp	
590 595 600	
cga tat gct aac cgg aat gtt gtc ttt ttt gat atc aac atg aaa ggt	1997
Arg Tyr Ala Asn Arg Asn Val Val Phe Phe Asp Ile Asn Met Lys Gly	
605 610 615	
ttg gat ggt att cag ggt cca att tat gtt ggt act gga tgt gta ttt	2045
Leu Asp Gly Ile Gln Gly Pro Ile Tyr Val Gly Thr Gly Cys Val Phe	
620 625 630	
aga agg cag gca tta tat ggt tat gat gcc ccc aaa aca aag aag cca	2093
Arg Arg Gln Ala Leu Tyr Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro	
635 640 645 650	
cca tca agg act tgc aac tgc tgg ccc aag tgg tgc ttt tgc tgt tgc	2141
Pro Ser Arg Thr Cys Asn Cys Trp Pro Lys Trp Cys Phe Cys Cys Cys	
655 660 665	
tgc ttt ggc aat agg aag caa aag aag act acc aaa ccc aaa aca gag	2189
Cys Phe Gly Asn Arg Lys Gln Lys Lys Thr Thr Lys Pro Lys Thr Glu	
670 675 680	
aag aaa aag tta tta ttt ttc aag aaa gaa gag aac caa tcc cct gca	2237
Lys Lys Lys Leu Leu Phe Phe Lys Lys Glu Glu Asn Gln Ser Pro Ala	
685 690 695	
tat gct ctt ggt gaa att gac gaa gct gct cca gga gct gag aat gaa	2285
Tyr Ala Leu Gly Glu Ile Asp Glu Ala Ala Pro Gly Ala Glu Asn Glu	
700 705 710	
aag gcc ggt att gta aat caa caa aaa tta gaa aag aaa ttt ggc caa	2333
Lys Ala Gly Ile Val Asn Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln	
715 720 725 730	
tct tct gtt ttt gtt aca tcc aca ctt ctc gag aat ggt gga acc ttg	2381
Ser Ser Val Phe Val Thr Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu	
735 740 745	
aag agt gca agt cct gct tct ctt ttg aaa gaa gct ata cat gtc att	2429
Lys Ser Ala Ser Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile	
750 755 760	
agt tgt ggt tat gaa gac aag aca gac tgg gga aaa gag att ggc tgg	2477
Ser Cys Gly Tyr Glu Asp Lys Thr Asp Trp Gly Lys Glu Ile Gly Trp	
765 770 775	
atc tat gga tca gtt aca gaa gat att cta act ggt ttc aag atg cat	2525
Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His	

- 36 -

780	785	790	
tgt cat ggt tgg cgg tca att tac tgc ata cct aaa cgg gtt gca ttc Cys His Gly Trp Arg Ser Ile Tyr Cys Ile Pro Lys Arg Val Ala Phe 795 800 805 810			2573
aaa ggt tct gca cct ctg aat ctt tca gat cgt ctt cac cag gtg ctt Lys Gly Ser Ala Pro Leu Asn Leu Ser Asp Arg Leu His Gln Val Leu 815 820 825			2621
cgg tgg gct ctt ggg tct att gag atc ttc ttc agc aat cat tgc cct Arg Trp Ala Leu Gly Ser Ile Glu Ile Phe Phe Ser Asn His Cys Pro 830 835 840			2669
ctt tgg tat ggg tat ggt ggc ggt ctg aaa ttt ttg gaa aga ttt tcc Leu Trp Tyr Gly Tyr Gly Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser 845 850 855			2717
tac atc aac tcc atc gtg tat cct tgg aca tct att ccc ctc ttg gct Tyr Ile Asn Ser Ile Val Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala 860 865 870			2765
tac tgt aca ttg cct gcc atc tgt tta ttg aca ggg aaa ttt atc act Tyr Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr 875 880 885 890			2813
cca gag ctg aat aat gtt gcc agc ctg tgg ttc atg tca ctt ttt atc Pro Glu Leu Asn Asn Val Ala Ser Leu Trp Phe Met Ser Leu Phe Ile 895 900 905			2861
tgc att ttt gct acg agc atc cta gaa atg aga tgg agt ggt gtt gga Cys Ile Phe Ala Thr Ser Ile Leu Glu Met Arg Trp Ser Gly Val Gly 910 915 920			2909
att gat gac tgg tgg agg aat gag cag ttc tgg gtc att gga ggt gtg Ile Asp Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val 925 930 935			2957
tcc tca cac ctc ttt gct gtg ttc cag gga ctt ctc aag gtc ata gct Ser Ser His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Ile Ala 940 945 950			3005
ggt gtt gat aca agc ttc acc gtg aca tca aag ggt gga gat gat gag Gly Val Asp Thr Ser Phe Thr Val Thr Ser Lys Gly Gly Asp Asp Glu 955 960 965 970			3053
gag ttc tca gag cta tat aca ttc aaa tgg act acc tta ttg ata cct Glu Phe Ser Glu Leu Tyr Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro 975 980 985			3101
cct acc acc ttg ctt cta ttg aac ttc att ggt gtg gtc gct ggc gtt Pro Thr Thr Leu Leu Leu Leu Asn Phe Ile Gly Val Val Ala Gly Val 990 995 1000			3149
tca aat gcg atc aat aac gga tat gag tca tgg ggc ccc ctc ttt ggg Ser Asn Ala Ile Asn Asn Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly 1005 1010 1015			3197

- 37 -

aag cta ttc ttt gca ttt tgg gtg att gtc cat ctt tat ccc ttt ctc 3245
 Lys Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu
 1020 1025 1030

aaa ggt ttg gtt gga agg caa aac agg aca cca acg att gtc atc gtc 3293
 Lys Gly Leu Val Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val
 1035 1040 1045 1050

tgg tcc att ctg ctg gct tca atc ttc tgg ctc ctt tgg gtt cgg att 3341
 Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile
 1055 1060 1065

gat cct ttc ctt gcg aag gat gat ggt ccg ctt ctt gag gag tgt ggt 3389
 Asp Pro Phe Leu Ala Lys Asp Asp Gly Pro Leu Leu Glu Glu Cys Gly
 1070 1075 1080

ttg gat tgc a actaggatgt cagtgcacat gtcaccccaa tctgcatatg 3439
 Leu Asp Cys
 1085

cttgaagtat attttctggt gtttgcctcc atattcagtg tctgtagata agagacatga 3499
 aatgtcccaa gtttcttttg atccatggtg aacctactta atatctgaga gatatactgg 3559
 gggaaaaatgg aggctgcggc aatccttctg cagttggggc gtggaataca gcatatgcaa 3619
 gtgtttgatt gtgcagcatt ctttattact tggtcgcaat atagatgggc tgagccgaac 3679
 agcaaggtat tttgattctg cactgctccc gtgtacaaac ttggttctca ataaggcagg 3739
 caggaatgca tctgccagtg gaacagagca acctgcacat tatttatgta tgcctgttca 3799
 ttggagggtt tgttcattac atgttcgtct atactagaaa aaacagaata ttagcattaa 3859
 tctatagtta attaaagtat gtaaatgcgc ctgttttttg ttgtgtactg taatcatctg 3919
 agttggtttt gtgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3969

<210> 18
 <211> 1086
 <212> PRT
 <213> Zea mays

<400> 18
 Met Glu Ala Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 Leu Val Val Ile Arg Arg Asp Gly Asp Pro Gly Pro Lys Pro Pro Arg
 20 25 30
 Glu Gln Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Asp Val Gly Leu
 35 40 45
 Ala Pro Gly Gly Asp Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro
 50 55 60
 Val Cys Arg Asp Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn
 65 70 75 80
 Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Leu Lys Gly Cys Gln Arg
 85 90 95
 Val Thr Gly Asp Glu Glu Glu Asp Gly Val Asp Asp Leu Asp Asn Glu
 100 105 110
 Phe Asn Trp Asp Gly His Asp Ser Gln Ser Val Ala Glu Ser Met Leu
 115 120 125
 Tyr Gly His Met Ser Tyr Gly Arg Gly Gly Asp Pro Asn Gly Ala Pro
 130 135 140
 Gln Ala Phe Gln Leu Asn Pro Asn Val Pro Leu Leu Thr Asn Gly Gln
 145 150 155 160
 Met Val Asp Asp Ile Pro Pro Glu Gln His Ala Leu Val Pro Ser Phe
 165 170 175

- 38 -

Met Gly Gly Gly Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro
 180 185 190
 Ser Leu Pro Val Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala
 195 200 205
 Ala Tyr Gly Tyr Gly Ser Val Ala Trp Lys Glu Arg Met Glu Asn Trp
 210 215 220
 Lys Gln Arg Gln Glu Arg Met His Gln Thr Gly Asn Asp Gly Gly Gly
 225 230 235 240
 Asp Asp Gly Asp Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln
 245 250 255
 Gln Leu Ser Arg Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr
 260 265 270
 Arg Met Ile Ile Ile Ile Arg Leu Val Val Leu Gly Phe Phe Phe His
 275 280 285
 Tyr Arg Val Met His Pro Val Asn Asp Ala Phe Ala Leu Trp Leu Ile
 290 295 300
 Ser Val Ile Cys Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln
 305 310 315 320
 Phe Pro Lys Trp Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu
 325 330 335
 Ser Leu Arg Phe Asp Lys Glu Gly Gln Pro Ser Gln Leu Ala Pro Ile
 340 345 350
 Asp Phe Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val
 355 360 365
 Thr Thr Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp
 370 375 380
 Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe
 385 390 395 400
 Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe
 405 410 415
 Cys Lys Arg Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln
 420 425 430
 Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Ala Ala Asn Phe Val Arg
 435 440 445
 Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile
 450 455 460
 Asn Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr
 465 470 475 480
 Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro
 485 490 495
 Gly Met Ile Gln Val Phe Leu Gly Gln Ser Gly Gly Leu Asp Cys Glu
 500 505 510
 Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro
 515 520 525
 Gly Tyr Asn His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg
 530 535 540
 Val Ser Ala Val Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys
 545 550 555 560
 Asp His Tyr Ile Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe
 565 570 575
 Met Met Asp Pro Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro
 580 585 590
 Gln Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn
 595 600 605
 Val Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly
 610 615 620
 Pro Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu Tyr
 625 630 635 640

- 39 -

Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro Pro Ser Arg Thr Cys Asn
 645 650 655
 Cys Trp Pro Lys Trp Cys Phe Cys Cys Cys Cys Phe Gly Asn Arg Lys
 660 665 670
 Gln Lys Lys Thr Thr Lys Pro Lys Thr Glu Lys Lys Lys Leu Leu Phe
 675 680 685
 Phe Lys Lys Glu Glu Asn Gln Ser Pro Ala Tyr Ala Leu Gly Glu Ile
 690 695 700
 Asp Glu Ala Ala Pro Gly Ala Glu Asn Glu Lys Ala Gly Ile Val Asn
 705 710 715 720
 Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln Ser Ser Val Phe Val Thr
 725 730 735
 Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu Lys Ser Ala Ser Pro Ala
 740 745 750
 Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp
 755 760 765
 Lys Thr Asp Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr
 770 775 780
 Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys His Gly Trp Arg Ser
 785 790 795 800
 Ile Tyr Cys Ile Pro Lys Arg Val Ala Phe Lys Gly Ser Ala Pro Leu
 805 810 815
 Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly Ser
 820 825 830
 Ile Glu Ile Phe Phe Ser Asn His Cys Pro Leu Trp Tyr Gly Tyr Gly
 835 840 845
 Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser Tyr Ile Asn Ser Ile Val
 850 855 860
 Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Leu Pro Ala
 865 870 875 880
 Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr Pro Glu Leu Asn Asn Val
 885 890 895
 Ala Ser Leu Trp Phe Met Ser Leu Phe Ile Cys Ile Phe Ala Thr Ser
 900 905 910
 Ile Leu Glu Met Arg Trp Ser Gly Val Gly Ile Asp Asp Trp Trp Arg
 915 920 925
 Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ser His Leu Phe Ala
 930 935 940
 Val Phe Gln Gly Leu Leu Lys Val Ile Ala Gly Val Asp Thr Ser Phe
 945 950 955 960
 Thr Val Thr Ser Lys Gly Gly Asp Asp Glu Glu Phe Ser Glu Leu Tyr
 965 970 975
 Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Leu
 980 985 990
 Leu Asn Phe Ile Gly Val Val Ala Gly Val Ser Asn Ala Ile Asn Asn
 995 1000 1005
 Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe
 1010 1015 1020
 Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Val Gly Arg
 1025 1030 1035 1040
 Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu Leu Ala
 1045 1050 1055
 Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Leu Ala Lys
 1060 1065 1070
 Asp Asp Gly Pro Leu Leu Glu Glu Cys Gly Leu Asp Cys Asn
 1075 1080 1085

- 40 -

<211> 25
 <212> DNA
 <213> Zea mays

<400> 19
 atggaggcga gcgcgggct ggtgg
 25

<210> 20
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 20
 ctagtgtcaa tccaaaccac actcc
 25

<210> 21
 <211> 3725
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (179)...(3398)

<400> 21
 gcagcagcag caccaccact gcgcggcatt gcagcgagca agcgggaggg atctggggca 60
 tggtaggggt cgctgccgct gccgctcgga tctagagggc cgcacgggct gattgccctc 120
 cgccggcctc gtcggtgtcg gtggagtgtg aatcgggtgtg ttaggagga gcgcggag 178
 atg gcg gcc aac aag ggg atg gtg gca ggc tct cac aac cgc aac gag 226
 Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 ttc gtc atg atc cgc cac gac ggc gac gcg cct gtc ccg gct aag ccc 274
 Phe Val Met Ile Arg His Asp Gly Asp Ala Pro Val Pro Ala Lys Pro
 20 25 30
 acg aag agt gcg aat ggg cag gtc tgc cag att tgt ggc gac act gtt 322
 Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Thr Val
 35 40 45
 ggc gtt tca gcc act ggt gat gtc ttt gtt gcc tgc aat gag tgt gcc 370
 Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys Ala
 50 55 60
 ttc cct gtc tgc cgc cct tgc tat gag tac gag cgc aag gaa ggg aac 418
 Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly Asn
 65 70 75 80
 caa tgc tgc cct cag tgc aag act aga tac aag aga cag aaa ggt agc 466
 Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser
 85 90 95
 cct cga gtt cat ggt gat gat gag gag gaa gat gtt gat gac ctg gac 514
 Pro Arg Val His Gly Asp Asp Glu Glu Glu Asp Val Asp Asp Leu Asp
 100 105 110

- 41 -

aat gaa ttc aac tat aag caa ggc aat ggg aag ggc cca gag tgg cag	562
Asn Glu Phe Asn Tyr Lys Gln Gly Asn Gly Lys Gly Pro Glu Trp Gln	
115 120 125	
ctt caa gga gat gac gct gat ctg tct tca tct gct cgc cat gac cca	610
Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Asp Pro	
130 135 140	
cac cat cgg att cca cgc ctt aca agt gga caa cag ata tct gga gag	658
His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly Glu	
145 150 155 160	
atc cct gat gca tcc cct gac cgt cat tct atc cgc agt cca aca tcg	706
Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr Ser	
165 170 175	
agc tat gtt gat cca agc gtt cca gtt cct gtg agg att gtg gac ccc	754
Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp Pro	
180 185 190	
tcg aag gac ttg aat tcc tat ggg ctt aat agt gtt gac tgg aag gaa	802
Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys Glu	
195 200 205	
aga gtt gag agc tgg agg gtt aaa cag gac aaa aat atg ttg caa gtg	850
Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Leu Gln Val	
210 215 220	
act aat aaa tat cca gag gct aga gga gac atg gag ggg act ggc tca	898
Thr Asn Lys Tyr Pro Glu Ala Arg Gly Asp Met Glu Gly Thr Gly Ser	
225 230 235 240	
aat gga gaa gat atg caa atg gtt gat gat gca cgc cta cct ttg agc	946
Asn Gly Glu Asp Met Gln Met Val Asp Asp Ala Arg Leu Pro Leu Ser	
245 250 255	
cgc att gtg cca att tcc tca aac cag ctc aac ctt tac cgg ata gta	994
Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg Ile Val	
260 265 270	
atc att ctc cgt ctt atc atc ctg tgc ttc ttc ttc caa tat cgt atc	1042
Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr Arg Ile	
275 280 285	
agt cat cca gtg cgt aat gct tat gga ttg tgg cta gta tct gtt atc	1090
Ser His Pro Val Arg Asn Ala Tyr Gly Leu Trp Leu Val Ser Val Ile	
290 295 300	
tgt gag gtc tgg ttt gcc ttg tcc tgg ctt cta gat cag ttc cca aaa	1138
Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe Pro Lys	
305 310 315 320	
tgg tat cca atc aac cgt gag aca tat ctc gac agg ctt gca ttg agg	1186
Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu Arg	
325 330 335	
tat gat aga gag gga gag cca tca cag ctg gct ccc att gat gtc ttt	1234
Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp Val Phe	

- 42 -

340	345	350	
gtc agt aca gtg gat cca ttg aag gaa cct cca ctg atc aca gcc aac			1282
Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala Asn			
355	360	365	
act gtt ttg tcc att ctt gct gtg gat tac cct gtt gac aaa gtg tca			1330
Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser			
370	375	380	
tgc tat gtt tct gat gat ggc tca gct atg ctg act ttt gag tct ctc			1378
Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser Leu			
385	390	395	400
tct gaa act gcc gaa ttt gct aga aag tgg gtt ccc ttt tgt aag aag			1426
Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys			
405	410	415	
cac aat att gaa cca aga gct cca gaa ttt tac ttt gct caa aaa ata			1474
His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln Lys Ile			
420	425	430	
gat tac ctg aag gac aaa att caa cct tca ttt gtt aag gaa aga cga			1522
Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg Arg			
435	440	445	
gca atg aag aga gag tat gaa gaa ttc aaa ata aga atc aat gcc ctt			1570
Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile Arg Ile Asn Ala Leu			
450	455	460	
gtt gcc aaa gca cag aaa gtg cct gaa gag ggg tgg acc atg gct gat			1618
Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Ala Asp			
465	470	475	480
gga act gct tgg cct ggg aat aac cct agg gac cat cct ggc atg att			1666
Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile			
485	490	495	
cag gtg ttc ttg ggg cac agt ggt ggg ctt gac act gat gga aat gaa			1714
Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn Glu			
500	505	510	
tta cca cgt ott gtc tat gtc tct cgt gaa aag aga cca ggc ttt cag			1762
Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln			
515	520	525	
cat cac aag aag gct ggt gca atg aat gca ctg att cgt gta tct gct			1810
His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala			
530	535	540	
gtg ctg aca aat ggt gcc tat ctt ctc aat gtg gat tgt gac cat tac			1858
Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His Tyr			
545	550	555	560
ttc aat agc agc aaa gct ctt aga gaa gca atg tgc ttc atg atg gat			1906
Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met Asp			
565	570	575	

- 43 -

cca gct cta gga agg aaa act tgt tat gta caa ttt cca caa aga ttt	1954
Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg Phe	
580 585 590	
gat ggc att gac ttg cac gat cga tat gct aat agg aac ata gtc ttc	2002
Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val Phe	
595 600 605	
ttt gat atc aac atg aaa ggt cta gat ggc att cag ggt cca gtc tat	2050
Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr	
610 615 620	
gtg gga aca gga tgc tgt ttc aat agg cag gct ttg tat gga tat gat	2098
Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr Asp	
625 630 635 640	
cct gtt ttg act gaa gct gat ctg gaa cct aac att gtt gtt aag agc	2146
Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Val Lys Ser	
645 650 655	
tgc tgt ggt aga agg aag aga aag aac aag agt tat atg gat agt caa	2194
Cys Cys Gly Arg Arg Lys Arg Lys Asn Lys Ser Tyr Met Asp Ser Gln	
660 665 670	
agc cgt att atg aag aga aca gaa tct tca gct ccc atc ttt aac atg	2242
Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe Asn Met	
675 680 685	
gaa gac atc gag gag ggt att gaa ggt tat gag gat gaa agg tca gtg	2290
Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg Ser Val	
690 695 700	
ctt atg tcc cag agg aaa ttg gag aaa cgc ttt ggt cag tct cca atc	2338
Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser Pro Ile	
705 710 715 720	
ttc att gca tcc acc ttt atg act caa ggt ggc ata cca cct tca aca	2386
Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro Ser Thr	
725 730 735	
aac cca gct tct cta ctg aag gaa gct atc cat gtt atc agc tgt ggg	2434
Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly	
740 745 750	
tac gag gac aaa act gaa tgg gga aaa gag att ggc tgg atc tat ggt	2482
Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly	
755 760 765	
tca gtt aca gag gat att ctg act ggg ttt aaa atg cat gca aga ggc	2530
Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly	
770 775 780	
tgg caa tca atc tac tgc atg cca cca cga cct tgt ttc aag ggt tct	2578
Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser	
785 790 795 800	
gca cca atc aat ctt tct gat cgt ctt aat cag gtg ctc cgt tgg gct	2626
Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala	

- 44 -

805	810	815	
ctt ggg tca gtg gaa att ctg ctt agc aga cat tgt cct ata tgg tat			2674
Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile Trp Tyr			
820	825	830	
ggc tac aat ggg cga ttg aag ctt ttg gag agg ctg gct tac att aac			2722
Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr Ile Asn			
835	840	845	
acc att gtt tat cca atc aca tct gtt ccg ctt atc gcc tat tgt gtg			2770
Thr Ile Val Tyr Pro Ile Thr Ser Val Pro Leu Ile Ala Tyr Cys Val			
850	855	860	
ctt cct gct atc tgt ctt ctt acc aat aaa ttt atc att cct gag att			2818
Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile			
865	870	875	880
agt aat tat gct gga atg ttc ttc att ctt ctt ttt gcc tcc att ttc			2866
Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser Ile Phe			
885	890	895	
gca act ggt ata ttg gag ctc aga tgg agt ggt gtt ggc att gaa gat			2914
Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp			
900	905	910	
tgg tgg aga aat gag cag ttt tgg gtt att ggt ggc acc tct gcc cat			2962
Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His			
915	920	925	
ctc ttc gcg gtg ttc cag ggt ctg ctg aaa gtg ttg gct ggg att gat			3010
Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp			
930	935	940	
acc aac ttc aca gtt acc tca aag gca tct gat gag gat ggc gac ttt			3058
Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp Phe			
945	950	955	960
gct gag cta tat gtg ttc aag tgg acc agt ttg ctc atc cct ccg acc			3106
Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr			
965	970	975	
act gtt ctt gtc att aac ctg gtc gga atg gtg gca gga att tcg tat			3154
Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr			
980	985	990	
gcc att aac agc ggc tac caa tcc tgg ggt ccg ctc ttt gga aag ctg			3202
Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu			
995	1000	1005	
ttc ttc tcg atc tgg gtg atc ctc cat ctc tac ccc ttc ctc aag ggt			3250
Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly			
1010	1015	1020	
ctc atg ggc agg cag aac cgc acg cca aca atc gtc atc gtt tgg tcc			3298
Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser			
1025	1030	1035	1040

- 45 -

atc ctc ctt gcg tct atc ttc tcc ttg ctg tgg gtg aag atc gat cct 3346
 Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro
 1045 1050 1055

ttc atc tcc ccg aca cag aaa gct gcc gcc ttg ggg caa tgt ggt gtg 3394
 Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys Gly Val
 1060 1065 1070

aac t gctgatccag attgtgactc ttatctgaag aggctcagcc aaagatctgc 3448
 Asn

cccctcgtgt aaatacctga gggggctaga tgggaatttt ttgttgtaga tgaggatgga 3508
 tctgcatcca agttatgcct ctgtttatta gcttcttcgg tgccggtgct gctgcagaca 3568
 atcatggagc ctttctacct tgctttagt gctggccagc agcgtaaatt gtgaattctg 3628
 cattttttta tacgtggtgt ttattgtttt agagtaaatt atcatttgtt tgaggtaact 3688
 attcacaga actatatggc aatgctgtta tttaaaa 3725

<210> 22
 <211> 1074
 <212> PRT
 <213> Zea mays

<400> 22

Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 Phe Val Met Ile Arg His Asp Gly Asp Ala Pro Val Pro Ala Lys Pro
 20 25 30
 Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Thr Val
 35 40 45
 Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys Ala
 50 55 60
 Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly Asn
 65 70 75 80
 Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser
 85 90 95
 Pro Arg Val His Gly Asp Asp Glu Glu Glu Asp Val Asp Asp Leu Asp
 100 105 110
 Asn Glu Phe Asn Tyr Lys Gln Gly Asn Gly Lys Gly Pro Glu Trp Gln
 115 120 125
 Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Asp Pro
 130 135 140
 His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly Glu
 145 150 155 160
 Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr Ser
 165 170 175
 Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp Pro
 180 185 190
 Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys Glu
 195 200 205
 Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Leu Gln Val
 210 215 220
 Thr Asn Lys Tyr Pro Glu Ala Arg Gly Asp Met Glu Gly Thr Gly Ser
 225 230 235 240
 Asn Gly Glu Asp Met Gln Met Val Asp Asp Ala Arg Leu Pro Leu Ser
 245 250 255
 Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg Ile Val
 260 265 270

- 46 -

Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr Arg Ile
 275 280 285
 Ser His Pro Val Arg Asn Ala Tyr Gly Leu Trp Leu Val Ser Val Ile
 290 295 300
 Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe Pro Lys
 305 310 315 320
 Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu Arg
 325 330 335
 Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp Val Phe
 340 345 350
 Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala Asn
 355 360 365
 Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser
 370 375 380
 Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser Leu
 385 390 395 400
 Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys
 405 410 415
 His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln Lys Ile
 420 425 430
 Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg Arg
 435 440 445
 Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile Arg Ile Asn Ala Leu
 450 455 460
 Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Ala Asp
 465 470 475 480
 Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile
 485 490 495
 Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn Glu
 500 505 510
 Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln
 515 520 525
 His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala
 530 535 540
 Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His Tyr
 545 550 555 560
 Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met Asp
 565 570 575
 Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg Phe
 580 585 590
 Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val Phe
 595 600 605
 Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr
 610 615 620
 Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr Asp
 625 630 635 640
 Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Val Lys Ser
 645 650 655
 Cys Cys Gly Arg Arg Lys Arg Lys Asn Lys Ser Tyr Met Asp Ser Gln
 660 665 670
 Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe Asn Met
 675 680 685
 Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg Ser Val
 690 695 700
 Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser Pro Ile
 705 710 715 720
 Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro Ser Thr
 725 730 735

- 47 -

Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly
 740 745 750
 Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly
 755 760 765
 Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly
 770 775 780
 Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser
 785 790 795 800
 Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala
 805 810 815
 Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile Trp Tyr
 820 825 830
 Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr Ile Asn
 835 840 845
 Thr Ile Val Tyr Pro Ile Thr Ser Val Pro Leu Ile Ala Tyr Cys Val
 850 855 860
 Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile
 865 870 875 880
 Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser Ile Phe
 885 890 895
 Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp
 900 905 910
 Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His
 915 920 925
 Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp
 930 935 940
 Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp Phe
 945 950 955 960
 Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr
 965 970 975
 Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr
 980 985 990
 Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu
 995 1000 1005
 Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly
 1010 1015 1020
 Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser
 1025 1030 1035 1040
 Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro
 1045 1050 1055
 Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys Gly Val
 1060 1065 1070
 Asn Cys

<210> 23
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 23
 atggcgccca acaaggggat ggtgg
 25

<210> 24
 <211> 25
 <212> DNA
 <213> Zea mays

- 48 -

<400> 24
tcagcagttc acaccacatt gcccc
25

<210> 25
<211> 3813
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (215) ... (3494)

<400> 25
ccacagctca tataccaaga gccggagcag cttagcgcag cccagagcgg cgccgcgccca 60
agcacaaccc ccaccgccca cagccgcgtg cgcattgtgag cggtcgccgc gcccgggaga 120
ccagaggagg ggaggactac gtgcatttcg ctgtgccgcc gcccggggggt tcgtgcgcga 180
gcgagatccg gcggggcggg gcggggggcc tgag atg gag gct agc gcg ggg ctg 235
Met Glu Ala Ser Ala Gly Leu
1 5

gtg gcc ggc tcg cat aac cgg aac gag ctg gtg gtg atc cgc cgc gac 283
Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg Arg Asp
10 15 20

cgc gag tcg gga gcc gcg ggc ggc ggc gcg gcg cgc cgg gcg gag gcg 331
Arg Glu Ser Gly Ala Ala Gly Gly Ala Ala Arg Arg Ala Glu Ala
25 30 35

ccg tgc cag ata tgc ggc gac gag gtc ggg gtg ggc ttc gac ggg gag 379
Pro Cys Gln Ile Cys Gly Asp Glu Val Gly Val Gly Phe Asp Gly Glu
40 45 50 55

ccc ttc gtg gcg tgc aac gag tgc gcc ttc ccc gtc tgc cgc gcc tgc 427
Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Val Cys Arg Ala Cys
60 65 70

tac gag tac gag cgc cgc gag ggc tcg caa gcg tgc ccg cag tgc agg 475
Tyr Glu Tyr Glu Arg Arg Glu Gly Ser Gln Ala Cys Pro Gln Cys Arg
75 80 85

acc cgc tac aag cgc ctc aag ggc tgc ccg cgg gtg gcc ggc gac gag 523
Thr Arg Tyr Lys Arg Leu Lys Gly Cys Pro Arg Val Ala Gly Asp Glu
90 95 100

gag gag gac ggc gtc gac gac ctg gag ggc gag ttc ggc ctg cag gac 571
Glu Glu Asp Gly Val Asp Asp Leu Glu Gly Glu Phe Gly Leu Gln Asp
105 110 115

ggc gcc gcc cac gag gac gac ccg cag tac gtc gcc gag tcc atg ctc 619
Gly Ala Ala His Glu Asp Asp Pro Gln Tyr Val Ala Glu Ser Met Leu
120 125 130 135

agg gcg cag atg agc tac ggc cgc ggc ggc gac gcg cac ccc ggc ttc 667
Arg Ala Gln Met Ser Tyr Gly Arg Gly Gly Asp Ala His Pro Gly Phe
140 145 150

- 49 -

agc ccc gtc ccc aac gtg ccg ctc ctc acc aac ggc cag atg gtt gat Ser Pro Val Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp 155 160 165	715
gac atc ccg ccg gag cag cac gcg ctc gtg ccg tcc tac atg agc ggc Asp Ile Pro Pro Glu Gln His Ala Leu Val Pro Ser Tyr Met Ser Gly 170 175 180	763
ggc ggc ggc ggc ggc aag agg atc cac ccg ctc cct ttc gca gat ccc Gly Gly Gly Gly Gly Lys Arg Ile His Pro Leu Pro Phe Ala Asp Pro 185 190 195	811
aac ctt cca gtg caa ccg aga tcc atg gac ccg tcc aag gat ctg gcc Asn Leu Pro Val Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala 200 205 210 215	859
gcc tac gga tat ggc agc gtg gcc tgg aag gag aga atg gag ggc tgg Ala Tyr Gly Tyr Gly Ser Val Ala Trp Lys Glu Arg Met Glu Gly Trp 220 225 230	907
aag cag aag cag gag cgc ctg cag cat gtc agg agc gag ggt ggc ggt Lys Gln Lys Gln Glu Arg Leu Gln His Val Arg Ser Glu Gly Gly Gly 235 240 245	955
gat tgg gat ggc gac gat gca gat ctg cca cta atg gat gaa gct agg Asp Trp Asp Gly Asp Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg 250 255 260	1003
cag cca ttg tcc aga aaa gtc cct ata tca tca agc cga att aat ccc Gln Pro Leu Ser Arg Lys Val Pro Ile Ser Ser Ser Arg Ile Asn Pro 265 270 275	1051
tac agg atg att atc gtt atc cgg ttg gtg gtt ttg ggt ttc ttc ttc Tyr Arg Met Ile Ile Val Ile Arg Leu Val Val Leu Gly Phe Phe Phe 280 285 290 295	1099
cac tac cga gtg atg cat ccg gcg aaa gat gca ttt gca ttg tgg ctc His Tyr Arg Val Met His Pro Ala Lys Asp Ala Phe Ala Leu Trp Leu 300 305 310	1147
ata tct gta atc tgt gaa atc tgg ttt gcg atg tcc tgg att ctt gat Ile Ser Val Ile Cys Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp 315 320 325	1195
cag ttc cca aag tgg ctt cca atc gag aga gag act tac ctg gac cgt Gln Phe Pro Lys Trp Leu Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg 330 335 340	1243
ttg tca cta agg ttt gac aag gaa ggt caa ccc tct cag ctt gct cca Leu Ser Leu Arg Phe Asp Lys Glu Gly Gln Pro Ser Gln Leu Ala Pro 345 350 355	1291
atc gac ttc ttt gtc agt acg gtt gat ccc aca aag gaa cct ccc ttg Ile Asp Phe Phe Val Ser Thr Val Asp Pro Thr Lys Glu Pro Pro Leu 360 365 370 375	1339
gtc aca gcg aac act gtc ctt tcc atc ctt tct gtg gat tat ccg gtt Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val	1387

- 50 -

380	385	390	
gag aag gtc tcc tgc tat gtt tct	gat gat ggt gct gca atg ctt acg		1435
Glu Lys Val Ser Cys Tyr Val Ser	Asp Asp Gly Ala Ala Met Leu Thr		
395	400	405	
ttt gaa gca ttg tct gaa aca tct	gaa ttt gca aag aaa tgg gtt cct		1483
Phe Glu Ala Leu Ser Glu Thr Ser	Glu Phe Ala Lys Lys Trp Val Pro		
410	415	420	
ttc agc aaa aag ttt aat atc gag	cct cgt gct cct gag tgg tac ttc		1531
Phe Ser Lys Lys Phe Asn Ile Glu	Pro Arg Ala Pro Glu Trp Tyr Phe		
425	430	435	
caa cag aag ata gac tac ctg aaa	gac aag gtt gct gct tca ttt gtt		1579
Gln Gln Lys Ile Asp Tyr Leu Lys	Asp Lys Val Ala Ala Ser Phe Val		
440	445	450	455
agg gag agg agg gcg atg aag aga	gaa tac gag gaa ttc aag gta agg		1627
Arg Glu Arg Arg Ala Met Lys Arg	Glu Tyr Glu Glu Phe Lys Val Arg		
460	465	470	
atc aat gcc ttg gtt gca aaa gcc	caa aag gtt cct gag gaa gga tgg		1675
Ile Asn Ala Leu Val Ala Lys Ala	Gln Lys Val Pro Glu Glu Gly Trp		
475	480	485	
aca atg caa gat gga agc ccc tgg	cct gga aac aac gta cgc gat cat		1723
Thr Met Gln Asp Gly Ser Pro Trp	Pro Gly Asn Asn Val Arg Asp His		
490	495	500	
cct gga atg att cag gta ttc ctt	ggc caa agt ggc ggt cgt gat gtg		1771
Pro Gly Met Ile Gln Val Phe Leu	Gly Gln Ser Gly Gly Arg Asp Val		
505	510	515	
gaa gga aat gag ttg cct cgc ctg	gtt tat gtc tgc aga gaa aag agg		1819
Glu Gly Asn Glu Leu Pro Arg Leu	Val Tyr Val Ser Arg Glu Lys Arg		
520	525	530	535
cca ggt tat aac cat cac aag aag	gct ggt gcc atg aat gca ctg gtc		1867
Pro Gly Tyr Asn His His Lys Lys	Ala Gly Ala Met Asn Ala Leu Val		
540	545	550	
cgt gtc tct gct gtc tta tca aat	gct gca tac cta ttg aac ttg gac		1915
Arg Val Ser Ala Val Leu Ser Asn	Ala Ala Tyr Leu Leu Asn Leu Asp		
555	560	565	
tgt gat cac tac atc aac aat agc	aag gcc ata aaa gag gct atg tgt		1963
Cys Asp His Tyr Ile Asn Asn Ser	Lys Ala Ile Lys Glu Ala Met Cys		
570	575	580	
ttc atg atg gat cct ttg gtg ggg	aag aaa gtg tgc tat gta cag ttc		2011
Phe Met Met Asp Pro Leu Val Gly	Lys Lys Val Cys Tyr Val Gln Phe		
585	590	595	
cct cag agg ttt gat ggt att gac	aaa aat gat cga tac gct aac agg		2059
Pro Gln Arg Phe Asp Gly Ile Asp	Lys Asn Asp Arg Tyr Ala Asn Arg		
600	605	610	615

- 51 -

aac gtt gtc ttt ttt gac atc aac atg aaa ggt ttg gac ggt att caa Asn Val Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln 620 625 630	2107
gga ccc att tat gtg ggt act gga tgt gtt ttc aga cgg cag gca ctg Gly Pro Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu 635 640 645	2155
tat ggt tat gat gct cct aaa acg aag aag cca cca tca aga act tgc Tyr Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro Pro Ser Arg Thr Cys 650 655 660	2203
aac tgc tgg ccc aag tgg tgc ctc tct tgc tgc tgc agc agg aac aag Asn Cys Trp Pro Lys Trp Cys Leu Ser Cys Cys Cys Ser Arg Asn Lys 665 670 675	2251
aat aaa aag aag act aca aaa cca aag acg gag aag aag aaa aga tta Asn Lys Lys Lys Thr Thr Lys Pro Lys Thr Glu Lys Lys Lys Arg Leu 680 685 690 695	2299
ttt ttc aag aaa gca gaa aac cca tct cct gca tat gct ttg ggt gaa Phe Phe Lys Lys Ala Glu Asn Pro Ser Pro Ala Tyr Ala Leu Gly Glu 700 705 710	2347
att gat gaa ggt gct cca ggt gct gat atc gag aag gcc gga atc gta Ile Asp Glu Gly Ala Pro Gly Ala Asp Ile Glu Lys Ala Gly Ile Val 715 720 725	2395
aat caa cag aaa cta gag aag aaa ttt ggg cag tct tct gtt ttt gtc Asn Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln Ser Ser Val Phe Val 730 735 740	2443
gca tca aca ctt ctt gag aac gga ggg acc ctg aag agc gca agt cca Ala Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu Lys Ser Ala Ser Pro 745 750 755	2491
gct tct ctt ctg aag gaa gct ata cat gtt atc agc tgc ggc tac gaa Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu 760 765 770 775	2539
gac aag acc gac tgg gga aaa gag att ggc tgg att tac gga tcg atc Asp Lys Thr Asp Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly Ser Ile 780 785 790	2587
aca gag gat atc ttg act gga ttt aag atg cac tgc cat ggc tgg cgg Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys His Gly Trp Arg 795 800 805	2635
tct att tac tgc atc ccg aag cgg cct gca ttc aaa ggt tct gcg cct Ser Ile Tyr Cys Ile Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro 810 815 820	2683
ctg aac ctt tcc gac cgt ctt cac cag gtc ctt cgc tgg gcc ctt ggg Leu Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly 825 830 835	2731
tcc gtc gaa att ttc ttc agc aag cac tgc cca ctt tgg tac gga tac Ser Val Glu Ile Phe Phe Ser Lys His Cys Pro Leu Trp Tyr Gly Tyr	2779

- 52 -

840	845	850	855	
ggc ggc ggc cta aaa ttc ctg gaa agg ttt tct tat atc aac tcc atc				2827
Gly Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser Tyr Ile Asn Ser Ile				
	860	865	870	
gtt tat ccc tgg acg tcc att cct ctc ctg gct tac tgt acc ttg cct				2875
Val Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Leu Pro				
	875	880	885	
gcc atc tgc ctg ctc acg ggg aag ttt atc aca cca gag ctt acc aat				2923
Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr Pro Glu Leu Thr Asn				
	890	895	900	
gtc gcc agt atc tgg ttc atg gca ctt ttc atc tgc atc tcc gtg acc				2971
Val Ala Ser Ile Trp Phe Met Ala Leu Phe Ile Cys Ile Ser Val Thr				
	905	910	915	
ggc atc ctg gaa atg agg tgg agt ggc gtg gcc atc gac gac tgg tgg				3019
Gly Ile Leu Glu Met Arg Trp Ser Gly Val Ala Ile Asp Asp Trp Trp				
	920	925	930	935
agg aac gag cag ttc tgg gtc atc gga ggc gtt tcg gcg cat ctg ttc				3067
Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe				
	940	945	950	
gcg gtg ttc cag ggc ctg ctg aag gtg ttc gcc ggc atc gac acg agc				3115
Ala Val Phe Gln Gly Leu Leu Lys Val Phe Ala Gly Ile Asp Thr Ser				
	955	960	965	
ttc acc gtg acg tcg aag gcc ggg gac gac gag gag ttc tcg gag ctg				3163
Phe Thr Val Thr Ser Lys Ala Gly Asp Asp Glu Glu Phe Ser Glu Leu				
	970	975	980	
tac acg ttc aag tgg acc acc ctg ctg ata ccc ccg acc acg ctc ctc				3211
Tyr Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu				
	985	990	995	
ctg ctg aac ttc atc ggg gtg gtg gcc ggg atc tcg aac gcg atc aac				3259
Leu Leu Asn Phe Ile Gly Val Val Ala Gly Ile Ser Asn Ala Ile Asn				
	1000	1005	1010	1015
aac ggg tac gag tcg tgg ggc ccc ctg ttc ggg aag ctc ttc ttc gcc				3307
Asn Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala				
	1020	1025	1030	
ttc tgg gtg atc gtc cac ctg tac ccg ttc ctc aag ggt ctg gtg ggg				3355
Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Val Gly				
	1035	1040	1045	
agg cag aac agg acg ccg acg atc gtc atc gtc tgg tcc atc ctg ctg				3403
Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu Leu				
	1050	1055	1060	
gcc tcg atc ttc tcg ctc ctg tgg gtc cgc gtc gac ccg ttc ctc gcc				3451
Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Val Asp Pro Phe Leu Ala				
	1065	1070	1075	

- 53 -

aag agc aac ggc ccg ctc ctg gag gag tgt ggc ctg gac tgc a 3494
 Lys Ser Asn Gly Pro Leu Leu Glu Glu Cys Gly Leu Asp Cys
 1080 1085 1090

actgaagtgg gggccccctg tcactcgaag ttctgtcacg ggcgaattac gcctgatttt 3554
 ttgttgttgt tgttgttgga attctttgct gtagatagaa accacatgtc cacggcatct 3614
 ctgctgtgtc cattggagca ggagagaggt gcctgctgtc gtttgttgag taaattaaaa 3674
 gttttaaagt tatacagtga tgcacattcc agtgcccagt gtattccctt tttacagtct 3734
 gtatattagc gacaaaggac atattgggta ggagtttgat tcttttgtaa aaaaaaaaaa 3794
 aaaaaaaaaa aaaaaaaaaa 3813

<210> 26
 <211> 1094
 <212> PRT
 <213> Zea mays

<400> 26
 Met Glu Ala Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 Leu Val Val Ile Arg Arg Asp Arg Glu Ser Gly Ala Ala Gly Gly Gly
 20 25 30
 Ala Ala Arg Arg Ala Glu Ala Pro Cys Gln Ile Cys Gly Asp Glu Val
 35 40 45
 Gly Val Gly Phe Asp Gly Glu Pro Phe Val Ala Cys Asn Glu Cys Ala
 50 55 60
 Phe Pro Val Cys Arg Ala Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Ser
 65 70 75 80
 Gln Ala Cys Pro Gln Cys Arg Thr Arg Tyr Lys Arg Leu Lys Gly Cys
 85 90 95
 Pro Arg Val Ala Gly Asp Glu Glu Glu Asp Gly Val Asp Asp Leu Glu
 100 105 110
 Gly Glu Phe Gly Leu Gln Asp Gly Ala Ala His Glu Asp Asp Pro Gln
 115 120 125
 Tyr Val Ala Glu Ser Met Leu Arg Ala Gln Met Ser Tyr Gly Arg Gly
 130 135 140
 Gly Asp Ala His Pro Gly Phe Ser Pro Val Pro Asn Val Pro Leu Leu
 145 150 155 160
 Thr Asn Gly Gln Met Val Asp Asp Ile Pro Pro Glu Gln His Ala Leu
 165 170 175
 Val Pro Ser Tyr Met Ser Gly Gly Gly Gly Gly Lys Arg Ile His
 180 185 190
 Pro Leu Pro Phe Ala Asp Pro Asn Leu Pro Val Gln Pro Arg Ser Met
 195 200 205
 Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr Gly Ser Val Ala Trp
 210 215 220
 Lys Glu Arg Met Glu Gly Trp Lys Gln Lys Gln Glu Arg Leu Gln His
 225 230 235 240
 Val Arg Ser Glu Gly Gly Gly Asp Trp Asp Gly Asp Asp Ala Asp Leu
 245 250 255
 Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg Lys Val Pro Ile
 260 265 270
 Ser Ser Ser Arg Ile Asn Pro Tyr Arg Met Ile Ile Val Ile Arg Leu
 275 280 285
 Val Val Leu Gly Phe Phe Phe His Tyr Arg Val Met His Pro Ala Lys
 290 295 300
 Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys Glu Ile Trp Phe
 305 310 315 320
 Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Leu Pro Ile Glu

- 54 -

325 330 335
 Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe Asp Lys Glu Gly
 340 345 350
 Gln Pro Ser Gln Leu Ala Pro Ile Asp Phe Phe Val Ser Thr Val Asp
 355 360 365
 Pro Thr Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val Leu Ser Ile
 370 375 380
 Leu Ser Val Asp Tyr Pro Val Glu Lys Val Ser Cys Tyr Val Ser Asp
 385 390 395 400
 Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser Glu Thr Ser Glu
 405 410 415
 Phe Ala Lys Lys Trp Val Pro Phe Ser Lys Lys Phe Asn Ile Glu Pro
 420 425 430
 Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp Tyr Leu Lys Asp
 435 440 445
 Lys Val Ala Ala Ser Phe Val Arg Glu Arg Arg Ala Met Lys Arg Glu
 450 455 460
 Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln
 465 470 475 480
 Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly Ser Pro Trp Pro
 485 490 495
 Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln Val Phe Leu Gly
 500 505 510
 Gln Ser Gly Gly Arg Asp Val Glu Gly Asn Glu Leu Pro Arg Leu Val
 515 520 525
 Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His His Lys Lys Ala
 530 535 540
 Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Ser Asn Ala
 545 550 555 560
 Ala Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys
 565 570 575
 Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro Leu Val Gly Lys
 580 585 590
 Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Lys
 595 600 605
 Asn Asp Arg Tyr Ala Asn Arg Asn Val Val Phe Phe Asp Ile Asn Met
 610 615 620
 Lys Gly Leu Asp Gly Ile Gln Gly Pro Ile Tyr Val Gly Thr Gly Cys
 625 630 635 640
 Val Phe Arg Arg Gln Ala Leu Tyr Gly Tyr Asp Ala Pro Lys Thr Lys
 645 650 655
 Lys Pro Pro Ser Arg Thr Cys Asn Cys Trp Pro Lys Trp Cys Leu Ser
 660 665 670
 Cys Cys Cys Ser Arg Asn Lys Asn Lys Lys Lys Thr Thr Lys Pro Lys
 675 680 685
 Thr Glu Lys Lys Lys Arg Leu Phe Phe Lys Lys Ala Glu Asn Pro Ser
 690 695 700
 Pro Ala Tyr Ala Leu Gly Glu Ile Asp Glu Gly Ala Pro Gly Ala Asp
 705 710 715 720
 Ile Glu Lys Ala Gly Ile Val Asn Gln Gln Lys Leu Glu Lys Lys Phe
 725 730 735
 Gly Gln Ser Ser Val Phe Val Ala Ser Thr Leu Leu Glu Asn Gly Gly
 740 745 750
 Thr Leu Lys Ser Ala Ser Pro Ala Ser Leu Leu Lys Glu Ala Ile His
 755 760 765
 Val Ile Ser Cys Gly Tyr Glu Asp Lys Thr Asp Trp Gly Lys Glu Ile
 770 775 780
 Gly Trp Ile Tyr Gly Ser Ile Thr Glu Asp Ile Leu Thr Gly Phe Lys

- 55 -

785 790 795 800
 Met His Cys His Gly Trp Arg Ser Ile Tyr Cys Ile Pro Lys Arg Pro
 805 810 815
 Ala Phe Lys Gly Ser Ala Pro Leu Asn Leu Ser Asp Arg Leu His Gln
 820 825 830
 Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Phe Phe Ser Lys His
 835 840 845
 Cys Pro Leu Trp Tyr Gly Tyr Gly Gly Gly Leu Lys Phe Leu Glu Arg
 850 855 860
 Phe Ser Tyr Ile Asn Ser Ile Val Tyr Pro Trp Thr Ser Ile Pro Leu
 865 870 875 880
 Leu Ala Tyr Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe
 885 890 895
 Ile Thr Pro Glu Leu Thr Asn Val Ala Ser Ile Trp Phe Met Ala Leu
 900 905 910
 Phe Ile Cys Ile Ser Val Thr Gly Ile Leu Glu Met Arg Trp Ser Gly
 915 920 925
 Val Ala Ile Asp Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly
 930 935 940
 Gly Val Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val
 945 950 955 960
 Phe Ala Gly Ile Asp Thr Ser Phe Thr Val Thr Ser Lys Ala Gly Asp
 965 970 975
 Asp Glu Glu Phe Ser Glu Leu Tyr Thr Phe Lys Trp Thr Thr Leu Leu
 980 985 990
 Ile Pro Pro Thr Thr Leu Leu Leu Leu Asn Phe Ile Gly Val Val Ala
 995 1000 1005
 Gly Ile Ser Asn Ala Ile Asn Asn Gly Tyr Glu Ser Trp Gly Pro Leu
 1010 1015 1020
 Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr Pro
 1025 1030 1035 1040
 Phe Leu Lys Gly Leu Val Gly Arg Gln Asn Arg Thr Pro Thr Ile Val
 1045 1050 1055
 Ile Val Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val
 1060 1065 1070
 Arg Val Asp Pro Phe Leu Ala Lys Ser Asn Gly Pro Leu Leu Glu Glu
 1075 1080 1085
 Cys Gly Leu Asp Cys Asn
 1090

<210> 27
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 27
 atggaggcta gcgcggggct ggtgg
 25

<210> 28
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 28
 tcagttgcag tccaggccac actcc
 25

<400> 29																
c	t	a	g	g	a	t	c	a	a	c	c	g	t	c	g	60
c	g	a	c	a	g	c	g	a	a	c	a	c	a	c	t	120
g	t	c	c	t	t	t	t	c	t	c	t	c	c	c	c	180
a	c	t	a	g	c	a	g	c	a	c	a	c	c	c	c	240
t	c	t	c	g	g	g	a	c	t	c	c	c	c	c	c	300
t	c	t	c	g	g	c	g	a	c	a	c	c	c	c	c	353
Met Glu Gly Asp Ala Asp Gly Val Lys Ser Gly																
1					5					10						
a	g	g	c	g	c	a	g	c	a	t	c	c	a	c	c	401
a	r	g	a	r	g	l	y	g	l	y	g	l	y	a	s	
15					20					25						
a	c	c	a	c	g	c	a	c	c	c	c	c	c	c	c	449
t	h	r	t	h	r	a	l	a	g	l	y	a	s	p	v	
30					35					40						
c	c	g	c	c	c	c	c	c	c	c	c	c	c	c	c	497
p	r	o	v	a	l	c	y	s	a	r	g	p	r	o	c	
45					50					55						
g	c	g	c	c	c	c	a	g	c	a	c	c	a	c	c	545
a	l	a	c	y	s	p	r	o	g	l	y	a	s	p	v	
60					65					70						
g	c	g	c	c	c	c	c	c	c	c	c	c	c	c	c	593
a	l	a	i	e	a	r	g	g	l	y	a	s	p	v	a	
80					85					90						
a	a	t	t	a	c	c	t	t	a	c	c	a	c	c	c	641
a	s	n	t	y	r	l	e	u	a	l	a	s	e	r	g	
95					100					105						
a	a	c	a	c	c	a	c	c	a	c	c	c	c	c	c	689
a	r	g	m	e	t	a	r	g	s	e	r	t	r	p	a	
110					115					120						
c	c	c	a	a	g	a	t	a	c	a	c	a	a	g	a	737
a	r	g	p	r	o	l	y	s	t	y	r	a	s	p	v	
125					130					135						
g	c	c	a	a	c	c	c	c	c	c	c	c	c	c	c	785
g	l	y	g	l	y	a	s	p	v	a	s	p	v	a	s	
140					145					150						
t	c	a	g	a	a	c	a	c	a	c	c	c	c	c	c	833
s	e	r	g	l	y	a	s	p	v	a	s	p	v	a	s	
160					165					170						

- 57 -

act ggg aac att ggc aag cgt gct cca ttt ccc tat gtg aac cat tcg Thr Gly Asn Ile Gly Lys Arg Ala Pro Phe Pro Tyr Val Asn His Ser 175 180 185	881
cca aat ccg tca agg gag ttc tct ggt agc att ggg aat gtt gcc tgg Pro Asn Pro Ser Arg Glu Phe Ser Gly Ser Ile Gly Asn Val Ala Trp 190 195 200	929
aaa gag agg gtt gat ggc tgg aaa atg aag cag gac aag ggg acg att Lys Glu Arg Val Asp Gly Trp Lys Met Lys Gln Asp Lys Gly Thr Ile 205 210 215	977
ccc atg acg aat ggc aca agc att gct ccc tct gag ggt cgg ggt gtt Pro Met Thr Asn Gly Thr Ser Ile Ala Pro Ser Glu Gly Arg Gly Val 220 225 230 235	1025
ggt gat att gat gca tca act gat tac aac atg gaa gat gcc tta ttg Gly Asp Ile Asp Ala Ser Thr Asp Tyr Asn Met Glu Asp Ala Leu Leu 240 245 250	1073
aac gac gaa act cga cag cct cta tct agg aaa gtt cca ctt cct tcc Asn Asp Glu Thr Arg Gln Pro Leu Ser Arg Lys Val Pro Leu Pro Ser 255 260 265	1121
tcc agg ata aat cca tac agg atg gtc att gtg ctg cga ttg att gtt Ser Arg Ile Asn Pro Tyr Arg Met Val Ile Val Leu Arg Leu Ile Val 270 275 280	1169
cta agc atc ttc ttg cac tac cgt atc aca aat cct gtg cgc aat gca Leu Ser Ile Phe Leu His Tyr Arg Ile Thr Asn Pro Val Arg Asn Ala 285 290 295	1217
tac cca tta tgg ctt cta tct gtt ata tgt gag atc tgg ttt gct ctt Tyr Pro Leu Trp Leu Leu Ser Val Ile Cys Glu Ile Trp Phe Ala Leu 300 305 310 315	1265
tcg tgg ata ttg gat cag ttc cct aag tgg ttt cca atc aac cgg gag Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Phe Pro Ile Asn Arg Glu 320 325 330	1313
acg tac ctt gat agg ctg gca tta agg tat gac cgg gaa ggt gag cca Thr Tyr Leu Asp Arg Leu Ala Leu Arg Tyr Asp Arg Glu Gly Glu Pro 335 340 345	1361
tct cag ttg gct gct gtt gac att ttc gtc agt aca gtc gac cca atg Ser Gln Leu Ala Ala Val Asp Ile Phe Val Ser Thr Val Asp Pro Met 350 355 360	1409
aag gag cct cct ctt gtc act gcc aat acc gtg cta tcc att ctt gct Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ala 365 370 375	1457
gtg gat tac cct gtg gat aag gtc tct tgc tat gta tct gat gat gga Val Asp Tyr Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly 380 385 390 395	1505
gct gcg atg ctg aca ttt gat gca cta gct gag act tca gag ttt gct	1553

- 58 -

Ala Ala Met Leu Thr Phe Asp Ala Leu Ala Glu Thr Ser Glu Phe Ala	
400 405 410	
aga aaa tgg gta cca ttt gtt aag aag tac aac att gaa cct aga gct	1601
Arg Lys Trp Val Pro Phe Val Lys Lys Tyr Asn Ile Glu Pro Arg Ala	
415 420 425	
cct gaa tgg tac ttc tcc cag aaa att gat tac ttg aag gac aaa gtg	1649
Pro Glu Trp Tyr Phe Ser Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val	
430 435 440	
cac cct tca ttt gtt aaa gac cgc cgg gcc atg aag aga gaa tat gaa	1697
His Pro Ser Phe Val Lys Asp Arg Arg Ala Met Lys Arg Glu Tyr Glu	
445 450 455	
gaa ttc aaa gtt agg gta aat ggc ctt gtt gct aag gca cag aaa gtt	1745
Glu Phe Lys Val Arg Val Asn Gly Leu Val Ala Lys Ala Gln Lys Val	
460 465 470 475	
cct gag gaa gga tgg atc atg caa gat ggc aca cca tgg cca gga aac	1793
Pro Glu Glu Gly Trp Ile Met Gln Asp Gly Thr Pro Trp Pro Gly Asn	
480 485 490	
aat acc mgg gac cat cct gga atg att cag gtt ttc ctt ggt cac agt	1841
Asn Thr Xaa Asp His Pro Gly Met Ile Gln Val Phe Leu Gly His Ser	
495 500 505	
ggt ggc ctt gat act gag ggc aat gag cta ccc cgt ttg gtc tat gtt	1889
Gly Gly Leu Asp Thr Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val	
510 515 520	
tct cgt gaa aag cgt cct gga ttc cag cat cac aag aaa gct ggt gcc	1937
Ser Arg Glu Lys Arg Pro Gly Phe Gln His His Lys Lys Ala Gly Ala	
525 530 535	
atg aat gct ctt gtt cgt gtc tca gct gtg ctt acc aat gga caa tac	1985
Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Gly Gln Tyr	
540 545 550 555	
atg ttg aat ctt gat tgt gat cac tac att aac aac agt aag gct ctc	2033
Met Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Leu	
560 565 570	
agg gaa gct atg tgc ttc ctt atg gac cct aac cta gga agg agt gtc	2081
Arg Glu Ala Met Cys Phe Leu Met Asp Pro Asn Leu Gly Arg Ser Val	
575 580 585	
tgc tac gtc cag ttt ccc cag aga ttc gat ggc att gac agg aat gat	2129
Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp	
590 595 600	
cga tat gcc aac agg aac acc gtg ttt ttc gat att aac ttg aga ggt	2177
Arg Tyr Ala Asn Arg Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly	
605 610 615	
ctt gat ggc atc caa gga cca gtt tat gtc gga act ggc tgt gtt ttc	2225
Leu Asp Gly Ile Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe	
620 625 630 635	

aac cga aca gct cta tat ggt tat gag ccc cca att aag cag aag aag Asn Arg Thr Ala Leu Tyr Gly Tyr Glu Pro Pro Ile Lys Gln Lys Lys 640 645 650	2273
ggt ggt ttc ttg tca tca cta tgt ggc ggt agg aag aag gca agc aaa Gly Gly Phe Leu Ser Ser Leu Cys Gly Gly Arg Lys Lys Ala Ser Lys 655 660 665	2321
tca aag aag ggc tcg gac aag aag aag tcg cag aag cat gtg gac agt Ser Lys Lys Gly Ser Asp Lys Lys Lys Ser Gln Lys His Val Asp Ser 670 675 680	2369
tct gtg cca gta ttc aac ctt gaa gat ata gag gag gga gtt gaa ggc Ser Val Pro Val Phe Asn Leu Glu Asp Ile Glu Glu Gly Val Glu Gly 685 690 695	2417
gct gga ttt gac gac gag aaa tca ctt ctt atg tct caa atg agc ctg Ala Gly Phe Asp Asp Glu Lys Ser Leu Leu Met Ser Gln Met Ser Leu 700 705 710 715	2465
gag aag aga ttt ggc cag tcc gca gcg ttt gtt gcc tcc act ctg atg Glu Lys Arg Phe Gly Gln Ser Ala Ala Phe Val Ala Ser Thr Leu Met 720 725 730	2513
gag tat ggt ggt gtt cct cag tcc gca act ccg gag tct ctt ctg aaa Glu Tyr Gly Val Pro Gln Ser Ala Thr Pro Glu Ser Leu Leu Lys 735 740 745	2561
gaa gct atc cat gtt ata agc tgt ggc tat gag gac aag act gaa tgg Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp 750 755 760	2609
gga act gag atc ggg tgg atc tac ggt tct gtg aca gaa gac att ctc Gly Thr Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu 765 770 775	2657
acc gga ttc aag atg cac gcg cga ggc tgg cgg tcg atc tac tgc atg Thr Gly Phe Lys Met His Ala Arg Gly Trp Arg Ser Ile Tyr Cys Met 780 785 790 795	2705
ccc aag cgg cca gct ttc aag ggg tct gcc ccc atc aat ctt tcg gac Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp 800 805 810	2753
cgt ctg aac cag gtg ctc cgg tgg gct ctt ggg tcc gtg gag atc ctc Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu 815 820 825	2801
ttc agc cgg cac tgc ccc ctg tgg tac ggc tac gga ggg cgg ctc aag Phe Ser Arg His Cys Pro Leu Trp Tyr Gly Tyr Gly Gly Arg Leu Lys 830 835 840	2849
ttc ctg gag aga ttc gcg tac atc aac acc acc atc tac ccg ctc acg Phe Leu Glu Arg Phe Ala Tyr Ile Asn Thr Thr Ile Tyr Pro Leu Thr 845 850 855	2897
tcc atc ccg ctt ctc atc tac tgc atc ctg ccc gcc atc tgt ctg ctc	2945

- 60 -

Ser Ile Pro Leu Leu Ile Tyr Cys Ile Leu Pro Ala Ile Cys Leu Leu	860	865	870	875	
acc gga aag ttc atc att cca gag atc agc aac ttc gcc agc atc tgg					2993
Thr Gly Lys Phe Ile Ile Pro Glu Ile Ser Asn Phe Ala Ser Ile Trp	880	885	890		
ttc atc tcc ctc ttc atc tcg atc ttc gcc acg ggc atc ctg gag atg					3041
Phe Ile Ser Leu Phe Ile Ser Ile Phe Ala Thr Gly Ile Leu Glu Met	895	900	905		
agg tgg agc ggg gtg ggc atc gac gag tgg tgg agg aac gag cag ttc					3089
Arg Trp Ser Gly Val Gly Ile Asp Glu Trp Trp Arg Asn Glu Gln Phe	910	915	920		
tgg gtg atc ggg ggc atc tcc gcg cac ctc ttc gcc gtg ttc cag ggc					3137
Trp Val Ile Gly Gly Ile Ser Ala His Leu Phe Ala Val Phe Gln Gly	925	930	935		
ctg ctc aag gtg ctg gcc ggc atc gac acc aac ttc acc gtc acc tcc					3185
Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser	940	945	950	955	
aag gcc tcg gac gag gac ggc gac ttc gcg gag ctg tac atg ttc aag					3233
Lys Ala Ser Asp Glu Asp Gly Asp Phe Ala Glu Leu Tyr Met Phe Lys	960	965	970		
tgg acg acg ctc ctg atc ccg ccc acc acc atc ctg atc atc aac ctg					3281
Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Ile Leu Ile Ile Asn Leu	975	980	985		
gtc ggc gtc gtc gcc ggc atc tcc tac gcc atc aac agc gga tac cag					3329
Val Gly Val Val Ala Gly Ile Ser Tyr Ala Ile Asn Ser Gly Tyr Gln	990	995	1000		
tcg tgg ggc ccg ctc ttc ggc aag ctc ttc ttc gcc ttc tgg gtc atc					3377
Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile	1005	1010	1015		
gtc cac ctg tac ccg ttc ctc aag ggc ctc atg ggc agg cag aac cgc					3425
Val His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg	1020	1025	1030	1035	
acc ccg acc atc gtc gtc gtc tgg gcc atc ctg ctg gcg tcc atc ttc					3473
Thr Pro Thr Ile Val Val Val Trp Ala Ile Leu Leu Ala Ser Ile Phe	1040	1045	1050		
tcc ttg ctg tgg gtt cgc atc gac ccc ttc acc acc cgc gtc act ggc					3521
Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Thr Thr Arg Val Thr Gly	1055	1060	1065		
ccg gat acc cag acg tgt ggc atc aac t gctaggaag tggaaggttt					3569
Pro Asp Thr Gln Thr Cys Gly Ile Asn	1070	1075			
gtacttttgta gaaacggagg aataccacgt gccatctggt gtctgttaag ttatatatat					3629
ataagcagca agtggcggtta tttacagcta cgtacagacc agtggatatt gtttaccaca					3689
aagtttttact tgtgttaata tgcattcttt tgttgatata aaaaaaaaaa aaaaaaa					3746

- 61 -

<210> 30
 <211> 1077
 <212> PRT
 <213> Zea mays

<400> 30

Met Glu Gly Asp Ala Asp Gly Val Lys Ser Gly Arg Arg Gly Gly Gly
 1 5 10 15
 Gln Val Cys Gln Ile Cys Gly Asp Gly Val Gly Thr Thr Ala Glu Gly
 20 25 30
 Asp Val Phe Ala Ala Cys Asp Val Cys Gly Phe Pro Val Cys Arg Pro
 35 40 45
 Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Thr Gln Ala Cys Pro Gln Cys
 50 55 60
 Lys Thr Lys Tyr Lys Arg His Lys Gly Ser Pro Ala Ile Arg Gly Glu
 65 70 75 80
 Glu Gly Asp Asp Thr Asp Ala Asp Ser Asp Phe Asn Tyr Leu Ala Ser
 85 90 95
 Gly Asn Glu Asp Gln Lys Gln Lys Ile Ala Asp Arg Met Arg Ser Trp
 100 105 110
 Arg Met Asn Val Gly Gly Ser Gly Asp Val Gly Arg Pro Lys Tyr Asp
 115 120 125
 Ser Gly Glu Ile Gly Leu Thr Lys Tyr Asp Ser Gly Glu Ile Pro Arg
 130 135 140
 Gly Tyr Ile Pro Ser Val Thr Asn Ser Gln Ile Ser Gly Glu Ile Pro
 145 150 155 160
 Gly Ala Ser Pro Asp His His Met Met Ser Pro Thr Gly Asn Ile Gly
 165 170 175
 Lys Arg Ala Pro Phe Pro Tyr Val Asn His Ser Pro Asn Pro Ser Arg
 180 185 190
 Glu Phe Ser Gly Ser Ile Gly Asn Val Ala Trp Lys Glu Arg Val Asp
 195 200 205
 Gly Trp Lys Met Lys Gln Asp Lys Gly Thr Ile Pro Met Thr Asn Gly
 210 215 220
 Thr Ser Ile Ala Pro Ser Glu Gly Arg Gly Val Gly Asp Ile Asp Ala
 225 230 235 240
 Ser Thr Asp Tyr Asn Met Glu Asp Ala Leu Leu Asn Asp Glu Thr Arg
 245 250 255
 Gln Pro Leu Ser Arg Lys Val Pro Leu Pro Ser Ser Arg Ile Asn Pro
 260 265 270
 Tyr Arg Met Val Ile Val Leu Arg Leu Ile Val Leu Ser Ile Phe Leu
 275 280 285
 His Tyr Arg Ile Thr Asn Pro Val Arg Asn Ala Tyr Pro Leu Trp Leu
 290 295 300
 Leu Ser Val Ile Cys Glu Ile Trp Phe Ala Leu Ser Trp Ile Leu Asp
 305 310 315 320
 Gln Phe Pro Lys Trp Phe Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg
 325 330 335
 Leu Ala Leu Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Ala
 340 345 350
 Val Asp Ile Phe Val Ser Thr Val Asp Pro Met Lys Glu Pro Pro Leu
 355 360 365
 Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val
 370 375 380
 Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr
 385 390 395 400
 Phe Asp Ala Leu Ala Glu Thr Ser Glu Phe Ala Arg Lys Trp Val Pro

- 62 -

405 410 415
 Phe Val Lys Lys Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe
 420 425 430
 Ser Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val His Pro Ser Phe Val
 435 440 445
 Lys Asp Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg
 450 455 460
 Val Asn Gly Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp
 465 470 475 480
 Ile Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Thr Xaa Asp His
 485 490 495
 Pro Gly Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr
 500 505 510
 Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg
 515 520 525
 Pro Gly Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val
 530 535 540
 Arg Val Ser Ala Val Leu Thr Asn Gly Gln Tyr Met Leu Asn Leu Asp
 545 550 555 560
 Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Leu Arg Glu Ala Met Cys
 565 570 575
 Phe Leu Met Asp Pro Asn Leu Gly Arg Ser Val Cys Tyr Val Gln Phe
 580 585 590
 Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp Arg Tyr Ala Asn Arg
 595 600 605
 Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly Leu Asp Gly Ile Gln
 610 615 620
 Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe Asn Arg Thr Ala Leu
 625 630 635 640
 Tyr Gly Tyr Glu Pro Ile Lys Gln Lys Lys Gly Gly Phe Leu Ser
 645 650 655
 Ser Leu Cys Gly Gly Arg Lys Lys Ala Ser Lys Ser Lys Lys Gly Ser
 660 665 670
 Asp Lys Lys Lys Ser Gln Lys His Val Asp Ser Ser Val Pro Val Phe
 675 680 685
 Asn Leu Glu Asp Ile Glu Glu Gly Val Glu Gly Ala Gly Phe Asp Asp
 690 695 700
 Glu Lys Ser Leu Leu Met Ser Gln Met Ser Leu Glu Lys Arg Phe Gly
 705 710 715 720
 Gln Ser Ala Ala Phe Val Ala Ser Thr Leu Met Glu Tyr Gly Gly Val
 725 730 735
 Pro Gln Ser Ala Thr Pro Glu Ser Leu Leu Lys Glu Ala Ile His Val
 740 745 750
 Ile Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Thr Glu Ile Gly
 755 760 765
 Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met
 770 775 780
 His Ala Arg Gly Trp Arg Ser Ile Tyr Cys Met Pro Lys Arg Pro Ala
 785 790 795 800
 Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val
 805 810 815
 Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu Phe Ser Arg His Cys
 820 825 830
 Pro Leu Trp Tyr Gly Tyr Gly Gly Arg Leu Lys Phe Leu Glu Arg Phe
 835 840 845
 Ala Tyr Ile Asn Thr Thr Ile Tyr Pro Leu Thr Ser Ile Pro Leu Leu
 850 855 860
 Ile Tyr Cys Ile Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile

- 63 -

865 870 875 880
 Ile Pro Glu Ile Ser Asn Phe Ala Ser Ile Trp Phe Ile Ser Leu Phe
 885 890 895
 Ile Ser Ile Phe Ala Thr Gly Ile Leu Glu Met Arg Trp Ser Gly Val
 900 905 910
 Gly Ile Asp Glu Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly
 915 920 925
 Ile Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu
 930 935 940
 Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu
 945 950 955 960
 Asp Gly Asp Phe Ala Glu Leu Tyr Met Phe Lys Trp Thr Thr Leu Leu
 965 970 975
 Ile Pro Pro Thr Thr Ile Leu Ile Ile Asn Leu Val Gly Val Val Ala
 980 985 990
 Gly Ile Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu
 995 1000 1005
 Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr Pro
 1010 1015 1020
 Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val
 1025 1030 1035 1040
 Val Val Trp Ala Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val
 1045 1050 1055
 Arg Ile Asp Pro Phe Thr Thr Arg Val Thr Gly Pro Asp Thr Gln Thr
 1060 1065 1070
 Cys Gly Ile Asn Cys
 1075

<210> 31
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 31
 atggagggcg acgcggacgg cgtga
 25

<210> 32
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 32
 ctagcagttg atgccacacg tctgg
 25

<210> 33
 <211> 3753
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (184)...(3406)

<400> 33
 cagcagcaga agcactgcgc ggcattgcag cgatcgagcg ggaggaattt ggggcatggt 60
 ggtcgccaac gccgctcgga tctagaggcc cgcacgggccc gattgggtctc cgcccgccctc 120

- 64 -

gtcgggtgttg gtgtcgttgg cgtgtggagc cgtctcggtg ggagcagcgg ggagggagcg	180
gag atg gcg gcc aac aag ggg atg gtg gcg ggc tcg cac aac cgc aac	228
Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn	
1 5 10 15	
gag ttc gtc atg atc cgc cac gac ggc gat gtg ccg ggc tcg gct aag	276
Glu Phe Val Met Ile Arg His Asp Gly Asp Val Pro Gly Ser Ala Lys	
20 25 30	
ccc aca aag agt gcg aat gga cag gtc tgc cag att tgc ggt gac tct	324
Pro Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Ser	
35 40 45	
gtg ggt gtt tca gcc act ggt gat gtc ttt gtt gcc tgc aat gag tgt	372
Val Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys	
50 55 60	
gcc ttc cct gtc tgc cgc cca tgc tat gag tat gag cgc aag gag ggg	420
Ala Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly	
65 70 75	
aac caa tgc tgc ccc cag tgc aag act aga tac aag aga cag aaa ggt	468
Asn Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly	
80 85 90 95	
agc cct cga gtt cat ggt gat gag gat gag gaa gat gtt gat gac cta	516
Ser Pro Arg Val His Gly Asp Glu Asp Glu Glu Asp Val Asp Asp Leu	
100 105 110	
gac aat gaa ttc aac tac aag caa ggc agt ggg aaa ggc cca gag tgg	564
Asp Asn Glu Phe Asn Tyr Lys Gln Gly Ser Gly Lys Gly Pro Glu Trp	
115 120 125	
caa ctg caa gga gat gat gct gat ctg tct tca tct gct cgc cat gag	612
Gln Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Glu	
130 135 140	
cca cat cat cgg att cca cgc ctg aca agc ggt caa cag ata tct gga	660
Pro His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly	
145 150 155	
gag att cct gat gct tcc cct gac cgt cat tct atc cgc agt cca aca	708
Glu Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr	
160 165 170 175	
tcg agc tat gtt gat cca agc gtc cca gtt cct gtg agg att gtg gac	756
Ser Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp	
180 185 190	
ccc tcg aag gac ttg aat tcc tat ggg ctt aat agt gtt gac tgg aag	804
Pro Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys	
195 200 205	
gaa aga gtt gag agc tgg agg gtt aaa cag gac aaa aat atg atg caa	852
Glu Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Met Gln	
210 215 220	
gtg act aat aaa tat cca gag gct aga gga gga gac atg gag ggg act	900

- 65 -

Val Thr Asn Lys Tyr Pro Glu Ala Arg Gly Gly Asp Met Glu Gly Thr	
225 230 235	
ggc tca aat gga gaa nat atg caa atg gtt gat gat gca cgg cta cct	948
Gly Ser Asn Gly Glu Xaa Met Gln Met Val Asp Asp Ala Arg Leu Pro	
240 245 250 255	
ttg agc cgt atc gtg cca att tcc tca aac cag ctc aac ctt tac cgg	996
Leu Ser Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg	
260 265 270	
gta gtg atc att ctc cgt ctt atc atc ctg tgc ttc ttc ttc cag tat	1044
Val Val Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr	
275 280 285	
cgt gtc agt cat cca gtg cgt gat gct tat gga tta tgg cta gta tct	1092
Arg Val Ser His Pro Val Arg Asp Ala Tyr Gly Leu Trp Leu Val Ser	
290 295 300	
gtt atc tgc gag gtc tgg ttt gcc ttg tct tgg ctt cta gat cag ttc	1140
Val Ile Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe	
305 310 315	
cca aaa tgg tat cca atc aac cgt gag aca tat ctt gac agg ctt gca	1188
Pro Lys Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala	
320 325 330 335	
ttg agg tat gat aga gag gga gag cca tca cag ctg gct ccc att gat	1236
Leu Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp	
340 345 350	
gtc ttc gtc agt aca gtg gat cca ttg aag gaa cct cca ctg atc aca	1284
Val Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr	
355 360 365	
gcc aac act gtt ttg tcc att ctt tct gtg gat tac cct gtt gac aaa	1332
Ala Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys	
370 375 380	
gtg tca tgc tat gtt tct gat gat ggt tca gct atg ctg act ttt gag	1380
Val Ser Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu	
385 390 395	
tct ctc tca gaa acc gca gaa ttt gct aga aag tgg gtt ccc ttt tgt	1428
Ser Leu Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys	
400 405 410 415	
aag aag cac aat att gaa cca aga gct cca gaa ttt tac ttt gct caa	1476
Lys Lys His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln	
420 425 430	
aaa ata gat tac ctg aag gac aaa att caa cct tca ttt gtt aag gaa	1524
Lys Ile Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu	
435 440 445	
aga cgc gca atg aag agg gag tat gaa gaa ttc aaa gta aga atc aat	1572
Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn	
450 455 460	

- 66 -

gcc ctt gtt gcc aaa gca cag aaa gtg cct gaa gag ggg tgg acc atg	1620
Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met	
465 470 475	
gct gat gga act gca tgg cct ggg aat aat cct agg gac cat cct ggc	1668
Ala Asp Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly	
480 485 490 495	
atg att cag gtt ttc ttg ggg cac agt ggt ggg ctc gac act gat gga	1716
Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly	
500 505 510	
aat gag tta cca cgt ctt gtc tat gtc tct cgt gaa aag aga cca ggc	1764
Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly	
515 520 525	
ttt cag cat cac aag aag gct ggt gca atg aat gcg ctg att cgt gta	1812
Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val	
530 535 540	
tct gct gtg ctg aca aat ggt gcc tat ctt ctc aat gtg gat tgc gac	1860
Ser Ala Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp	
545 550 555	
cat tac ttc aat agc agc aaa gct ctt aga gaa gca atg tgc ttc atg	1908
His Tyr Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met	
560 565 570 575	
atg gat ccg gct cta gga agg aaa act tgt tat gta caa ttt cca cag	1956
Met Asp Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln	
580 585 590	
aga ttt gat ggc att gac ttg cac gat cga tat gct aat cgg aac ata	2004
Arg Phe Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile	
595 600 605	
gtt ttc ttt gat atc aac atg aaa ggt ctg gat ggc att cag ggt cca	2052
Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro	
610 615 620	
gtt tac gtg gga aca gga tgc tgt ttc aat aga cag gct ttg tat gga	2100
Val Tyr Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly	
625 630 635	
tac gat cct gtt ttg act gaa gct gat ctg gag cca aac att gtt att	2148
Tyr Asp Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Ile	
640 645 650 655	
aag agc tgc tgt ggt aga agg aag aaa aag aac aag agt tat atg gat	2196
Lys Ser Cys Cys Gly Arg Arg Lys Lys Lys Asn Lys Ser Tyr Met Asp	
660 665 670	
agt caa agc cgt att atg aag aga aca gaa tct tca gct ccc atc ttc	2244
Ser Gln Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe	
675 680 685	
aat atg gaa gac atc gaa gag ggt att gaa ggt tac gag gat gaa agg	2292

- 67 -

Asn Met	Glu	Asp	Ile	Glu	Glu	Gly	Ile	Glu	Gly	Tyr	Glu	Asp	Glu	Arg	
	690					695					700				
tca gtg ctt atg tcc cag agg aaa ttg gag aaa cgc ttt ggt cag tct															2340
Ser Val Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser															
	705					710				715					
cct att ttc att gca tcc acc ttt atg aca caa ggt ggc ata cca cct															2388
Pro Ile Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro															
	720				725				730					735	
tca aca aac cca gct tct cta cta aag gaa gct atc cat gtc atc agt															2436
Ser Thr Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser															
				740				745					750		
tgt gga tat gag gac aaa act gaa tgg gga aaa gag att ggc tgg atc															2484
Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile															
				755				760					765		
tat ggt tca gta acg gag gat att ctg act ggg ttt aaa atg cat gca															2532
Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala															
				770				775					780		
agg ggc tgg caa tca atc tac tgc atg cca cca cga cct tgt ttc aag															2580
Arg Gly Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys															
				785				790					795		
ggt tct gca cca atc aat ctt tcc gat cgt ctt aat cag gtg ctc cgt															2628
Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg															
	800				805				810					815	
tgg gct ctt ggg tca gtg gaa att ctg ctt agt aga cat tgt cct atc															2676
Trp Ala Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile															
				820				825						830	
tgg tat ggt tac aat gga cga ttg aag ctt ttg gag agg ctg gct tac															2724
Trp Tyr Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr															
				835				840					845		
atc aac act att gta tat cca atc aca tcc att ccg ctt att gcc tat															2772
Ile Asn Thr Ile Val Tyr Pro Ile Thr Ser Ile Pro Leu Ile Ala Tyr															
				850				855					860		
tgt gtg ctt ccc gct atc tgc ctc ctt acc aat aaa ttt atc att cct															2820
Cys Val Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro															
				865				870					875		
gag att agc aat tat gct ggg atg ttc ttc att ctt ctt ttc gcc tcc															2868
Glu Ile Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser															
	880					885				890				895	
att ttt gcc act ggt ata ttg gag ctt aga tgg agt ggt gtt ggc att															2916
Ile Phe Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile															
				900				905						910	
gaa gat tgg tgg aga aat gag cag ttt tgg gtt att ggt ggc acc tct															2964
Glu Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser															
				915				920						925	

- 68 -

```

gcc cat ctc ttc gca gtg ttc cag ggt ctg ctg aaa gtg ttg gct ggg      3012
Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly
      930                      935                      940

att gat acc aac ttc aca gtt acc tca aag gca tct gat gag gat ggc      3060
Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly
      945                      950                      955

gac ttt gct gag cta tat gtg ttc aag tgg acc agt ttg ctc att cct      3108
Asp Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro
      960                      965                      970                      975

ccg acc act gtt ctt gtc att aac ctg gtc gga atg gtg gca gga att      3156
Pro Thr Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile
      980                      985                      990

tct tat gcc att aac agt ggc tac caa tcc tgg ggt ccg ctc ttt gga      3204
Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly
      995                      1000                      1005

aag ctg ttc ttc tcg atc tgg gtg atc ctc cat ctc tac ccc ttc ctc      3252
Lys Leu Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu
      1010                      1015                      1020

aag ggt ctc atg gga agg cag aac cgc aca cca aca atc gtc att gtc      3300
Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val
      1025                      1030                      1035

tgg tcc atc ctt ctt gca tct atc ttc tcc ttg ctg tgg gtg aag atc      3348
Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile
      1040                      1045                      1050                      1055

gat cct ttc atc tcc ccg aca cag aaa gct gct gcc ttg ggg caa tgt      3396
Asp Pro Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys
      1060                      1065                      1070

ggc gtc aac t gctgatcgag acagtgaactc ttatttgaag aggctcaatc      3446
Gly Val Asn

aagatctgcc ccctcgtgta aatacctgag gaggctagat gggaattcct tttgtttag      3506
gtgaggatgg atttgcattc aagttatgcc tctgttcatt agcttcttcc gtgccggtgc      3566
tgctgcggac taagaatcac ggagccttcc taccttccat gtagcgccag ccagcagcgt      3626
aagatgtgaa ttttgaagtt ttgttatgcg tgcagtttat tgttttagag taaattatca      3686
tttgtttgtg ggaactgttc acacgagctt ataatggcaa tgctgttatt taaaaaaaaa      3746
aaaaaaaaa      3753

<210> 34
<211> 1075
<212> PRT
<213> Zea mays

<400> 34
Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu
 1                      5                      10                      15
Phe Val Met Ile Arg His Asp Gly Asp Val Pro Gly Ser Ala Lys Pro
      20                      25                      30

```

- 69 -

Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Ser Val
 35 40 45
 Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys Ala
 50 55 60
 Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly Asn
 65 70 75 80
 Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser
 85 90 95
 Pro Arg Val His Gly Asp Glu Asp Glu Glu Asp Val Asp Asp Leu Asp
 100 105 110
 Asn Glu Phe Asn Tyr Lys Gln Gly Ser Gly Lys Gly Pro Glu Trp Gln
 115 120 125
 Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Glu Pro
 130 135 140
 His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly Glu
 145 150 155 160
 Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr Ser
 165 170 175
 Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp Pro
 180 185 190
 Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys Glu
 195 200 205
 Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Met Gln Val
 210 215 220
 Thr Asn Lys Tyr Pro Glu Ala Arg Gly Gly Asp Met Glu Gly Thr Gly
 225 230 235 240
 Ser Asn Gly Glu Xaa Met Gln Met Val Asp Asp Ala Arg Leu Pro Leu
 245 250 255
 Ser Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg Val
 260 265 270
 Val Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr Arg
 275 280 285
 Val Ser His Pro Val Arg Asp Ala Tyr Gly Leu Trp Leu Val Ser Val
 290 295 300
 Ile Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe Pro
 305 310 315 320
 Lys Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu
 325 330 335
 Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp Val
 340 345 350
 Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala
 355 360 365
 Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val
 370 375 380
 Ser Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser
 385 390 395 400
 Leu Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys
 405 410 415
 Lys His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln Lys
 420 425 430
 Ile Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg
 435 440 445
 Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala
 450 455 460
 Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Ala
 465 470 475 480
 Asp Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met
 485 490 495

- 70 -

Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn
 500 505 510
 Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe
 515 520 525
 Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser
 530 535 540
 Ala Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His
 545 550 555 560
 Tyr Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met
 565 570 575
 Asp Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg
 580 585 590
 Phe Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val
 595 600 605
 Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val
 610 615 620
 Tyr Val Gly Thr Gly Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr
 625 630 635 640
 Asp Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Ile Lys
 645 650 655
 Ser Cys Cys Gly Arg Arg Lys Lys Lys Asn Lys Ser Tyr Met Asp Ser
 660 665 670
 Gln Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe Asn
 675 680 685
 Met Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg Ser
 690 695 700
 Val Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser Pro
 705 710 715 720
 Ile Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro Ser
 725 730 735
 Thr Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys
 740 745 750
 Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr
 755 760 765
 Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg
 770 775 780
 Gly Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly
 785 790 795 800
 Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp
 805 810 815
 Ala Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile Trp
 820 825 830
 Tyr Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr Ile
 835 840 845
 Asn Thr Ile Val Tyr Pro Ile Thr Ser Ile Pro Leu Ile Ala Tyr Cys
 850 855 860
 Val Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu
 865 870 875 880
 Ile Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser Ile
 885 890 895
 Phe Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu
 900 905 910
 Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala
 915 920 925
 His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile
 930 935 940
 Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp
 945 950 955 960

- 71 -

Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro
 965 970 975
 Thr Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser
 980 985 990
 Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys
 995 1000 1005
 Leu Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys
 1010 1015 1020
 Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp
 1025 1030 1035 1040
 Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp
 1045 1050 1055
 Pro Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys Gly
 1060 1065 1070
 Val Asn Cys
 1075

<210> 35
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 35
 atggcgccca acaaggggat ggtgg
 25

<210> 36
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 36
 tcagcagttg acgccacatt gcccc
 25

<210> 37
 <211> 3969
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (144)...(3399)

<400> 37
 cttctccctc gtcggtgcgg cgtggcgcg ctcggcggttc ggtgagaaac cactcggggg 60
 atgaggatct gctgctagag tgagaggagc tacggtcagt atcctctgcc ttcgtcggcg 120
 gcggaagtgg aggggaggaa gcg atg gag gcg agc gcc ggg ctg gtg gcc ggc 173
 Met Glu Ala Ser Ala Gly Leu Val Ala Gly
 1 5 10

tcc cac aac cgc aac gag ctc gtc gtc atc cgc cgc gac ggc gat ccc 221
 Ser His Asn Arg Asn Glu Leu Val Val Ile Arg Arg Asp Gly Asp Pro
 15 20 25

ggg ccg aag ccg ccg cgg gag cag aac ggg cag gtg tgc cag att tgc 269
 Gly Pro Lys Pro Pro Arg Glu Gln Asn Gly Gln Val Cys Gln Ile Cys
 30 35 40

- 72 -

ggc gac gac gtc ggc ctt gcc ccc ggc ggg gac ccc ttc gtg gcg tgc Gly Asp Asp Val Gly Leu Ala Pro Gly Gly Asp Pro Phe Val Ala Cys 45 50 55	317
aac gag tgc gcc ttc ccc gtc tgc cgg gac tgc tac gaa tac gag cgc Asn Glu Cys Ala Phe Pro Val Cys Arg Asp Cys Tyr Glu Tyr Glu Arg 60 65 70	365
cgg gag ggc acg cag aac tgc ccc cag tgc aag act cga tac aag cgc Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg 75 80 85 90	413
ctc aag ggc tgc caa cgt gtg acc ggt gac gag gag gag gac ggc gtc Leu Lys Gly Cys Gln Arg Val Thr Gly Asp Glu Glu Glu Asp Gly Val 95 100 105	461
gat gac ctg gac aac gag ttc aac tgg gac ggc cat gac tcg cag tct Asp Asp Leu Asp Asn Glu Phe Asn Trp Asp Gly His Asp Ser Gln Ser 110 115 120	509
gtg gcc gag tcc atg ctc tac ggc cac atg agc tac ggc cgt gga ggt Val Ala Glu Ser Met Leu Tyr Gly His Met Ser Tyr Gly Arg Gly Gly 125 130 135	557
gac cct aat ggc gcg cca caa gct ttc cag ctc aac ccc aat gtt cca Asp Pro Asn Gly Ala Pro Gln Ala Phe Gln Leu Asn Pro Asn Val Pro 140 145 150	605
ctc ctc acc aac ggg caa atg gtg gat gac atc cca ccg gag cag cac Leu Leu Thr Asn Gly Gln Met Val Asp Asp Ile Pro Pro Glu Gln His 155 160 165 170	653
gcg ctg gtg cct tct ttc atg ggt ggt ggg gga aag agg ata cat ccc Ala Leu Val Pro Ser Phe Met Gly Gly Gly Lys Arg Ile His Pro 175 180 185	701
ctt cct tat gcg gat ccc agc tta cct gtg caa ccc agg tct atg gac Leu Pro Tyr Ala Asp Pro Ser Leu Pro Val Gln Pro Arg Ser Met Asp 190 195 200	749
cca tcc aag gat ctt gct gca tat ggg tat ggt agt gtt gct tgg aag Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr Gly Ser Val Ala Trp Lys 205 210 215	797
gaa cgg atg gag aat tgg aag cag aga caa gag agg atg cac cag acg Glu Arg Met Glu Asn Trp Lys Gln Arg Gln Glu Arg Met His Gln Thr 220 225 230	845
ggg aat gat ggt ggt ggt gat gat ggt gac gat gct gat cta cca cta Gly Asn Asp Gly Gly Gly Asp Asp Gly Asp Ala Asp Leu Pro Leu 235 240 245 250	893
atg gat gaa gca aga caa caa ctg tcc agg aaa att cca ctt cca tca Met Asp Glu Ala Arg Gln Gln Leu Ser Arg Lys Ile Pro Leu Pro Ser 255 260 265	941
agc cag att aat cca tat agg atg att atc att att cgg ctt gtg gtt	989

- 73 -

Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile Ile Ile Arg Leu Val Val	
270 275 280	
ttg ggg ttc ttc ttc cac tac cga gtg atg cat ccg gtg aat gat gca	1037
Leu Gly Phe Phe Phe His Tyr Arg Val Met His Pro Val Asn Asp Ala	
285 290 295	
ttt gct ttg tgg ctc ata tct gtt atc tgt gaa atc tgg ttt gcc atg	1085
Phe Ala Leu Trp Leu Ile Ser Val Ile Cys Glu Ile Trp Phe Ala Met	
300 305 310	
tct tgg att ctt gat caa ttc cca aag tgg ttc cct att gag aga gag	1133
Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Phe Pro Ile Glu Arg Glu	
315 320 325 330	
act tac cta gac cgg ctg tca ctg agg ttc gac aag gaa ggc cag cca	1181
Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe Asp Lys Glu Gly Gln Pro	
335 340 345	
tct caa ctt gct cca att gat ttc ttt gtc agt acg gtt gat ccc tta	1229
Ser Gln Leu Ala Pro Ile Asp Phe Phe Val Ser Thr Val Asp Pro Leu	
350 355 360	
aag gaa cct cct ttg gtc aca aca aat act gtt cta tct atc ctt tcg	1277
Lys Glu Pro Pro Leu Val Thr Thr Asn Thr Val Leu Ser Ile Leu Ser	
365 370 375	
gtg gat tat cct gtt gat aag gtt tct tgc tat gtt tct gat gat ggt	1325
Val Asp Tyr Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly	
380 385 390	
gct gca atg cta acg ttt gaa gca tta tct gaa aca tct gaa ttt gca	1373
Ala Ala Met Leu Thr Phe Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala	
395 400 405 410	
aag aaa tgg gtt cct ttc tgc aaa cgg tac aat att gaa cct cgc gct	1421
Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr Asn Ile Glu Pro Arg Ala	
415 420 425	
cca gag tgg tac ttc caa cag aag ata gac tac ttg aaa gac aag gtg	1469
Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val	
430 435 440	
gca gca aac ttt gtt agg gag agg aga gca atg aag aga gag tat gag	1517
Ala Ala Asn Phe Val Arg Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu	
445 450 455	
gaa ttc aag gtg aga atc aat gcc tta gtt gcc aaa gcc cag aaa gtt	1565
Glu Phe Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Val	
460 465 470	
cct gaa gaa gga tgg aca atg caa gat gga acc ccc tgg cct gga aac	1613
Pro Glu Glu Gly Trp Thr Met Gln Asp Gly Thr Pro Trp Pro Gly Asn	
475 480 485 490	
aat gtt cgt gat cat cct gga atg att cag gtc ttc ctt ggc caa agc	1661
Asn Val Arg Asp His Pro Gly Met Ile Gln Val Phe Leu Gly Gln Ser	
495 500 505	

- 74 -

gga ggc ctt gac tgt gag gga aat gaa ctg cca cga ttg gtt tat gtt Gly Gly Leu Asp Cys Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val 510 515 520	1709
tct aga gag aaa cga cca ggc tat aac cat cat aag aaa gct ggt gct Ser Arg Glu Lys Arg Pro Gly Tyr Asn His His Lys Lys Ala Gly Ala 525 530 535	1757
atg aat gca ttg gtc cga gtc tct gct gta cta aca aat gct cca tat Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Ala Pro Tyr 540 545 550	1805
ttg tta aac ttg gat tgt gat cac tac atc aac aac agc aag gct ata Leu Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Ile 555 560 565 570	1853
aag gaa gca atg tgt ttt atg atg gac cct tta cta gga aag aag gtt Lys Glu Ala Met Cys Phe Met Met Asp Pro Leu Leu Gly Lys Lys Val 575 580 585	1901
tgc tat gta cag ttc cct caa aga ttt gat ggg att gat cgc cat gac Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg His Asp 590 595 600	1949
cga tat gct aac cgg aat gtt gtc ttt ttt gat atc aac atg aaa ggt Arg Tyr Ala Asn Arg Asn Val Val Phe Phe Asp Ile Asn Met Lys Gly 605 610 615	1997
ttg gat ggt att cag ggt cca att tat gtt ggt act gga tgt gta ttt Leu Asp Gly Ile Gln Gly Pro Ile Tyr Val Gly Thr Gly Cys Val Phe 620 625 630	2045
aga agg cag gca tta tat ggt tat gat gcc ccc aaa aca aag aag cca Arg Arg Gln Ala Leu Tyr Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro 635 640 645 650	2093
cca tca agg act tgc aac tgc tgg ccc aag tgg tgc ttt tgc tgt tgc Pro Ser Arg Thr Cys Asn Cys Trp Pro Lys Trp Cys Phe Cys Cys Cys 655 660 665	2141
tgc ttt ggc aat agg aag caa aag aag act acc aaa ccc aaa aca gag Cys Phe Gly Asn Arg Lys Gln Lys Lys Thr Thr Lys Pro Lys Thr Glu 670 675 680	2189
aag aaa aag tta tta ttt ttc aag aaa gaa gag aac caa tcc cct gca Lys Lys Lys Leu Leu Phe Phe Lys Lys Glu Glu Asn Gln Ser Pro Ala 685 690 695	2237
tat gct ctt ggt gaa att gac gaa gct gct cca gga gct gag aat gaa Tyr Ala Leu Gly Glu Ile Asp Glu Ala Ala Pro Gly Ala Glu Asn Glu 700 705 710	2285
aag gcc ggt att gta aat caa caa aaa tta gaa aag aaa ttt ggc caa Lys Ala Gly Ile Val Asn Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln 715 720 725 730	2333
tct tct gtt ttt gtt aca tcc aca ctt ctc gag aat ggt gga acc ttg	2381

- 75 -

Ser Ser Val Phe Val Thr Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu	
735 740 745	
aag agt gca agt cct gct tct ctt ttg aaa gaa gct ata cat gtc att	2429
Lys Ser Ala Ser Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile	
750 755 760	
agt tgt ggt tat gaa gac aag aca gac tgg gga aaa gag att ggc tgg	2477
Ser Cys Gly Tyr Glu Asp Lys Thr Asp Trp Gly Lys Glu Ile Gly Trp	
765 770 775	
atc tat gga tca gtt aca gaa gat att cta act ggt ttc aag atg cat	2525
Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His	
780 785 790	
tgt cat ggt tgg cgg tca att tac tgc ata cct aaa cgg gtt gca ttc	2573
Cys His Gly Trp Arg Ser Ile Tyr Cys Ile Pro Lys Arg Val Ala Phe	
795 800 805 810	
aaa ggt tct gca cct ctg aat ctt tca gat cgt ctt cac cag gtg ctt	2621
Lys Gly Ser Ala Pro Leu Asn Leu Ser Asp Arg Leu His Gln Val Leu	
815 820 825	
cgg tgg gct ctt ggg tct att gag atc ttc ttc agc aat cat tgc cct	2669
Arg Trp Ala Leu Gly Ser Ile Glu Ile Phe Phe Ser Asn His Cys Pro	
830 835 840	
ctt tgg tat ggg tat ggt ggc ggt ctg aaa ttt ttg gaa aga ttt tcc	2717
Leu Trp Tyr Gly Tyr Gly Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser	
845 850 855	
tac atc aac tcc atc gtg tat cct tgg aca tct att ccc ctc ttg gct	2765
Tyr Ile Asn Ser Ile Val Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala	
860 865 870	
tac tgt aca ttg cct gcc atc tgt tta ttg aca ggg aaa ttt atc act	2813
Tyr Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr	
875 880 885 890	
cca gag ctg aat aat gtt gcc agc ctg tgg ttc atg tca ctt ttt atc	2861
Pro Glu Leu Asn Asn Val Ala Ser Leu Trp Phe Met Ser Leu Phe Ile	
895 900 905	
tgc att ttt gct acg agc atc cta gaa atg aga tgg agt ggt gtt gga	2909
Cys Ile Phe Ala Thr Ser Ile Leu Glu Met Arg Trp Ser Gly Val Gly	
910 915 920	
att gat gac tgg tgg agg aat gag cag ttc tgg gtc att gga ggt gtg	2957
Ile Asp Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val	
925 930 935	
tcc tca cac ctc ttt gct gtg ttc cag gga ctt ctc aag gtc ata gct	3005
Ser Ser His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Ile Ala	
940 945 950	
ggg gtt gat aca agc ttc acc gtg aca tca aag ggt gga gat gat gag	3053
Gly Val Asp Thr Ser Phe Thr Val Thr Ser Lys Gly Gly Asp Asp Glu	
955 960 965 970	

- 76 -

gag ttc tca gag cta tat aca ttc aaa tgg act acc tta ttg ata cct 3101
 Glu Phe Ser Glu Leu Tyr Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro
 975 980 985

cct acc acc ttg ctt cta ttg aac ttc att ggt gtg gtc gct ggc gtt 3149
 Pro Thr Thr Leu Leu Leu Leu Asn Phe Ile Gly Val Val Ala Gly Val
 990 995 1000

tca aat gcg atc aat aac gga tat gag tca tgg ggc ccc ctc ttt ggg 3197
 Ser Asn Ala Ile Asn Asn Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly
 1005 1010 1015

aag cta ttc ttt gca ttt tgg gtg att gtc cat ctt tat ccc ttt ctc 3245
 Lys Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu
 1020 1025 1030

aaa ggt ttg gtt gga agg caa aac agg aca cca acg att gtc atc gtc 3293
 Lys Gly Leu Val Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val
 1035 1040 1045 1050

tgg tcc att ctg ctg gct tca atc ttc tgc ctc ctt tgg gtt cgg att 3341
 Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile
 1055 1060 1065

gat cct ttc ctt gcg aag gat gat ggt ccg ctt ctt gag gag tgt ggt 3389
 Asp Pro Phe Leu Ala Lys Asp Asp Gly Pro Leu Leu Glu Glu Cys Gly
 1070 1075 1080

ttg gat tgc a actaggatgt cagtgcacat gctcccccaa tctgcatatg 3439
 Leu Asp Cys
 1085

cttgaagtat attttctggt gtttgtcccc atattcagtg tctgtagata agagacatga 3499
 aatgtcccaa gtttcttttg atccatggtg aacctactta atatctgaga gatatactgg 3559
 gggaaaatgg aggcgcggc aatccttggt cagttgggccc gtggaataca gcatatgcaa 3619
 gtgtttgatt gtgcagcatt ctttattact tggctgcgaat atagatgggc tgagccgaac 3679
 agcaaggat tttgattctg cactgctccc gtgtacaaac ttggttctca ataaggcagg 3739
 caggaatgca tctgccagt gaacagagca acctgcacat tatttatgta tgctgttca 3799
 ttggagggct tgttcattac atgttcgtct atactagaaa aaacagaata ttagcattaa 3859
 tctatagtta attaaagtat gtaaatgcgc ctgttttttg ttgtgtactg taatcatctg 3919
 agttggtttt gtgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3969

<210> 38

<211> 1086

<212> PRT

<213> Zea mays

<400> 38

Met Glu Ala Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 Leu Val Val Ile Arg Arg Asp Gly Asp Pro Gly Pro Lys Pro Pro Arg
 20 25 30
 Glu Gln Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Asp Val Gly Leu
 35 40 45
 Ala Pro Gly Gly Asp Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro
 50 55 60
 Val Cys Arg Asp Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn

- 77 -

65					70					75				80
Cys	Pro	Gln	Cys	Lys	Thr	Arg	Tyr	Lys	Arg	Leu	Lys	Gly	Cys	Gln
				85					90					95
Val	Thr	Gly	Asp	Glu	Glu	Glu	Asp	Gly	Val	Asp	Asp	Leu	Asp	Asn
			100					105					110	
Phe	Asn	Trp	Asp	Gly	His	Asp	Ser	Gln	Ser	Val	Ala	Glu	Ser	Met
		115					120					125		Leu
Tyr	Gly	His	Met	Ser	Tyr	Gly	Arg	Gly	Gly	Asp	Pro	Asn	Gly	Ala
	130					135				140				Pro
Gln	Ala	Phe	Gln	Leu	Asn	Pro	Asn	Val	Pro	Leu	Leu	Thr	Asn	Gly
145					150					155				160
Met	Val	Asp	Asp	Ile	Pro	Pro	Glu	Gln	His	Ala	Leu	Val	Pro	Ser
				165					170					175
Met	Gly	Gly	Gly	Gly	Lys	Arg	Ile	His	Pro	Leu	Pro	Tyr	Ala	Asp
			180				185					190		Pro
Ser	Leu	Pro	Val	Gln	Pro	Arg	Ser	Met	Asp	Pro	Ser	Lys	Asp	Leu
	195						200					205		Ala
Ala	Tyr	Gly	Tyr	Gly	Ser	Val	Ala	Trp	Lys	Glu	Arg	Met	Glu	Asn
	210				215						220			Trp
Lys	Gln	Arg	Gln	Glu	Arg	Met	His	Gln	Thr	Gly	Asn	Asp	Gly	Gly
225					230					235				240
Asp	Asp	Gly	Asp	Asp	Ala	Asp	Leu	Pro	Leu	Met	Asp	Glu	Ala	Arg
				245					250					255
Gln	Leu	Ser	Arg	Lys	Ile	Pro	Leu	Pro	Ser	Ser	Gln	Ile	Asn	Pro
			260				265					270		Tyr
Arg	Met	Ile	Ile	Ile	Ile	Arg	Leu	Val	Val	Leu	Gly	Phe	Phe	Phe
	275					280					285			His
Tyr	Arg	Val	Met	His	Pro	Val	Asn	Asp	Ala	Phe	Ala	Leu	Trp	Leu
	290				295					300				Ile
Ser	Val	Ile	Cys	Glu	Ile	Trp	Phe	Ala	Met	Ser	Trp	Ile	Leu	Asp
305					310				315					Gln
Phe	Pro	Lys	Trp	Phe	Pro	Ile	Glu	Arg	Glu	Thr	Tyr	Leu	Asp	Arg
			325						330					Leu
Ser	Leu	Arg	Phe	Asp	Lys	Glu	Gly	Gln	Pro	Ser	Gln	Leu	Ala	Pro
			340				345					350		Ile
Asp	Phe	Phe	Val	Ser	Thr	Val	Asp	Pro	Leu	Lys	Glu	Pro	Pro	Leu
	355					360					365			Val
Thr	Thr	Asn	Thr	Val	Leu	Ser	Ile	Leu	Ser	Val	Asp	Tyr	Pro	Val
	370				375					380				Asp
Lys	Val	Ser	Cys	Tyr	Val	Ser	Asp	Asp	Gly	Ala	Ala	Met	Leu	Thr
385					390				395					Phe
Glu	Ala	Leu	Ser	Glu	Thr	Ser	Glu	Phe	Ala	Lys	Lys	Trp	Val	Pro
				405					410					Phe
Cys	Lys	Arg	Tyr	Asn	Ile	Glu	Pro	Arg	Ala	Pro	Glu	Trp	Tyr	Phe
			420					425				430		Gln
Gln	Lys	Ile	Asp	Tyr	Leu	Lys	Asp	Lys	Val	Ala	Ala	Asn	Phe	Val
	435						440					445		Arg
Glu	Arg	Arg	Ala	Met	Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys	Val	Arg
	450				455				460					Ile
Asn	Ala	Leu	Val	Ala	Lys	Ala	Gln	Lys	Val	Pro	Glu	Glu	Gly	Trp
465					470				475					Thr
Met	Gln	Asp	Gly	Thr	Pro	Trp	Pro	Gly	Asn	Asn	Val	Arg	Asp	His
			485					490					495	Pro
Gly	Met	Ile	Gln	Val	Phe	Leu	Gly	Gln	Ser	Gly	Gly	Leu	Asp	Cys
			500				505					510		Glu
Gly	Asn	Glu	Leu	Pro	Arg	Leu	Val	Tyr	Val	Ser	Arg	Glu	Lys	Arg
	515					520					525			Pro
Gly	Tyr	Asn	His	His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ala	Leu	Val

- 78 -

530	535	540
Val Ser Ala Val Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys		
545	550	555
Asp His Tyr Ile Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe		560
	565	570
Met Met Asp Pro Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro		575
	580	585
Gln Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn		590
	595	600
Val Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly		605
	610	615
Pro Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu Tyr		620
	625	630
Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro Pro Ser Arg Thr Cys Asn		635
	645	650
Cys Trp Pro Lys Trp Cys Phe Cys Cys Cys Cys Phe Gly Asn Arg Lys		655
	660	665
Gln Lys Lys Thr Thr Lys Pro Lys Thr Glu Lys Lys Lys Leu Leu Phe		670
	675	680
Phe Lys Lys Glu Glu Asn Gln Ser Pro Ala Tyr Ala Leu Gly Glu Ile		685
	690	695
Asp Glu Ala Ala Pro Gly Ala Glu Asn Glu Lys Ala Gly Ile Val Asn		700
	705	710
Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln Ser Ser Val Phe Val Thr		715
	725	730
Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu Lys Ser Ala Ser Pro Ala		735
	740	745
Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp		750
	755	760
Lys Thr Asp Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr		765
	770	775
Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys His Gly Trp Arg Ser		780
	785	790
Ile Tyr Cys Ile Pro Lys Arg Val Ala Phe Lys Gly Ser Ala Pro Leu		795
	805	810
Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly Ser		815
	820	825
Ile Glu Ile Phe Phe Ser Asn His Cys Pro Leu Trp Tyr Gly Tyr Gly		830
	835	840
Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser Tyr Ile Asn Ser Ile Val		845
	850	855
Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Leu Pro Ala		860
	865	870
Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr Pro Glu Leu Asn Asn Val		875
	885	890
Ala Ser Leu Trp Phe Met Ser Leu Phe Ile Cys Ile Phe Ala Thr Ser		895
	900	905
Ile Leu Glu Met Arg Trp Ser Gly Val Gly Ile Asp Asp Trp Trp Arg		910
	915	920
Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ser His Leu Phe Ala		925
	930	935
Val Phe Gln Gly Leu Leu Lys Val Ile Ala Gly Val Asp Thr Ser Phe		940
	945	950
Thr Val Thr Ser Lys Gly Gly Asp Asp Glu Glu Phe Ser Glu Leu Tyr		955
	965	970
Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Leu		975
	980	985
Leu Asn Phe Ile Gly Val Val Ala Gly Val Ser Asn Ala Ile Asn Asn		990

- 79 -

995	1000	1005
Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe		
1010	1015	1020
Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Val Gly Arg		
1025	1030	1035
Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu Leu Ala		
1045	1050	1055
Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Leu Ala Lys		
1060	1065	1070
Asp Asp Gly Pro Leu Leu Glu Glu Cys Gly Leu Asp Cys Asn		
1075	1080	1085

<210> 39
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 39
 atggaggcga gcgccgggct ggtgg
 25

<210> 40
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 40
 ctagttgcaa tccaaaccac actcc
 25

<210> 41
 <211> 3725
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (179)...(3398)

<400> 41	
gcagcagcag caccaccact gcgcggcatt gcagcgagca agcgggaggg atctggggca	60
tggtggcggt cgctgccgct gccgctcgga tctagagggc cgcacgggct gattgccctc	120
cgccggcctc gtcggtgtcg gtggagtgtg aatcggtgtg ttagaggagga gcgcggag	178
atg gcg gcc aac aag ggg atg gtg gca ggc tct cac aac cgc aac gag	226
Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu	
1 5 10 15	
ttc gtc atg atc cgc cac gac ggc gac gcg cct gtc ccg gct aag ccc	274
Phe Val Met Ile Arg His Asp Gly Asp Ala Pro Val Pro Ala Lys Pro	
20 25 30	
acg aag agt gcg aat ggg cag gtc tgc cag att tgt ggc gac act gtt	322
Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Thr Val	
35 40 45	
ggc gtt tca gcc act ggt gat gtc ttt gtt gcc tgc aat gag tgt gcc	370
Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys Ala	
50 55 60	

- 80 -

ttc cct gtc tgc cgc cct tgc tat gag tac gag cgc aag gaa ggg aac	418
Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly Asn	
65 70 75 80	
caa tgc tgc cct cag tgc aag act aga tac aag aga cag aaa ggt agc	466
Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser	
85 90 95	
cct cga gtt cat ggt gat gat gag gag gaa gat gtt gat gac ctg gac	514
Pro Arg Val His Gly Asp Asp Glu Glu Glu Asp Val Asp Asp Leu Asp	
100 105 110	
aat gaa ttc aac tat aag caa ggc aat ggg aag ggc cca gag tgg cag	562
Asn Glu Phe Asn Tyr Lys Gln Gly Asn Gly Lys Gly Pro Glu Trp Gln	
115 120 125	
ctt caa gga gat gac gct gat ctg tct tca tct gct cgc cat gac cca	610
Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Asp Pro	
130 135 140	
cac cat cgg att cca cgc ctt aca agt gga caa cag ata tct gga gag	658
His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly Glu	
145 150 155 160	
atc cct gat gca tcc cct gac cgt cat tct atc cgc agt cca aca tcg	706
Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr Ser	
165 170 175	
agc tat gtt gat cca agc gtt cca gtt cct gtg agg att gtg gac ccc	754
Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp Pro	
180 185 190	
tcg aag gac ttg aat tcc tat ggg ctt aat agt gtt gac tgg aag gaa	802
Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys Glu	
195 200 205	
aga gtt gag agc tgg agg gtt aaa cag gac aaa aat atg ttg caa gtg	850
Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Leu Gln Val	
210 215 220	
act aat aaa tat cca gag gct aga gga gac atg gag ggg act ggc tca	898
Thr Asn Lys Tyr Pro Glu Ala Arg Gly Asp Met Glu Gly Thr Gly Ser	
225 230 235 240	
aat gga gaa gat atg caa atg gtt gat gat gca cgc cta cct ttg agc	946
Asn Gly Glu Asp Met Gln Met Val Asp Asp Ala Arg Leu Pro Leu Ser	
245 250 255	
cgc att gtg cca att tcc tca aac cag ctc aac ctt tac cgg ata gta	994
Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg Ile Val	
260 265 270	
atc att ctc cgt ctt atc atc ctg tgc ttc ttc ttc caa tat cgt atc	1042
Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr Arg Ile	
275 280 285	
agt cat cca gtg cgt aat gct tat gga ttg tgg cta gta tct gtt atc	1090

- 81 -

Ser His Pro Val Arg Asn Ala Tyr Gly Leu Trp Leu Val Ser Val Ile	
290 295 300	
tgt gag gtc tgg ttt gcc ttg tcc tgg ctt cta gat cag ttc cca aaa	1138
Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe Pro Lys	
305 310 315 320	
tgg tat cca atc aac cgt gag aca tat ctc gac agg ctt gca ttg agg	1186
Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu Arg	
325 330 335	
tat gat aga gag gga gag cca tca cag ctg gct ccc att gat gtc ttt	1234
Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp Val Phe	
340 345 350	
gtc agt aca gtg gat cca ttg aag gaa cct cca ctg atc aca gcc aac	1282
Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala Asn	
355 360 365	
act gtt ttg tcc att ctt gct gtg gat tac cct gtt gac aaa gtg tca	1330
Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser	
370 375 380	
tgc tat gtt tct gat gat ggc tca gct atg ctg act ttt gag tct ctc	1378
Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser Leu	
385 390 395 400	
tct gaa act gcc gaa ttt gct aga aag tgg gtt ccc ttt tgt aag aag	1426
Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys	
405 410 415	
cac aat att gaa cca aga gct cca gaa ttt tac ttt gct caa aaa ata	1474
His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln Lys Ile	
420 425 430	
gat tac ctg aag gac aaa att caa cct tca ttt gtt aag gaa aga cga	1522
Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg Arg	
435 440 445	
gca atg aag aga gag tat gaa gaa ttc aaa ata aga atc aat gcc ctt	1570
Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile Arg Ile Asn Ala Leu	
450 455 460	
gtt gcc aaa gca cag aaa gtg cct gaa gag ggg tgg acc atg gct gat	1618
Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Ala Asp	
465 470 475 480	
gga act gct tgg cct ggg aat aac cct agg gac cat cct ggc atg att	1666
Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile	
485 490 495	
cag gtg ttc ttg ggg cac agt ggt ggg ctt gac act gat gga aat gaa	1714
Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn Glu	
500 505 510	
tta cca cgt ctt gtc tat gtc tct cgt gaa aag aga cca ggc ttt cag	1762
Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln	
515 520 525	

- 82 -

cat cac aag aag gct ggt gca atg aat gca ctg att cgt gta tct gct His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala 530 535 540	1810
gtg ctg aca aat ggt gcc tat ctt ctc aat gtg gat tgt gac cat tac Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His Tyr 545 550 555 560	1858
ttc aat agc agc aaa gct ctt aga gaa gca atg tgc ttc atg atg gat Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met Asp 565 570 575	1906
cca gct cta gga agg aaa act tgt tat gta caa ttt cca caa aga ttt Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg Phe 580 585 590	1954
gat ggc att gac ttg cac gat cga tat gct aat agg aac ata gtc ttc Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val Phe 595 600 605	2002
ttt gat atc aac atg aaa ggt cta gat ggc att cag ggt cca gtc tat Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr 610 615 620	2050
gtg gga aca gga tgc tgt ttc aat agg cag gct ttg tat gga tat gat Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr Asp 625 630 635 640	2098
cct gtt ttg act gaa gct gat ctg gaa cct aac att gtt gtt aag agc Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Val Lys Ser 645 650 655	2146
tgc tgt ggt aga agg aag aga aag aac aag agt tat atg gat agt caa Cys Cys Gly Arg Arg Lys Arg Lys Asn Lys Ser Tyr Met Asp Ser Gln 660 665 670	2194
agc cgt att atg aag aga aca gaa tct tca gct ccc atc ttt aac atg Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe Asn Met 675 680 685	2242
gaa gac atc gag gag ggt att gaa ggt tat gag gat gaa agg tca gtg Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg Ser Val 690 695 700	2290
ctt atg tcc cag agg aaa ttg gag aaa cgc ttt ggt cag tct cca atc Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser Pro Ile 705 710 715 720	2338
ttc att gca tcc acc ttt atg act caa ggt ggc ata cca cct tca aca Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro Ser Thr 725 730 735	2386
aac cca gct tct cta ctg aag gaa gct atc cat gtt atc agc tgt ggg Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly 740 745 750	2434
tac gag gac aaa act gaa tgg gga aaa gag att ggc tgg atc tat ggt	2482

- 83 -

Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly	
755 760 765	
tca gtt aca gag gat att ctg act ggg ttt aaa atg cat gca aga ggc	2530
Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly	
770 775 780	
tgg caa tca atc tac tgc atg cca cca cga cct tgt ttc aag ggt tct	2578
Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser	
785 790 795 800	
gca cca atc aat ctt tct gat cgt ctt aat cag gtg ctc cgt tgg gct	2626
Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala	
805 810 815	
ctt ggg tca gtg gaa att ctg ctt agc aga cat tgt cct ata tgg tat	2674
Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile Trp Tyr	
820 825 830	
ggc tac aat ggg cga ttg aag ctt ttg gag agg ctg gct tac att aac	2722
Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr Ile Asn	
835 840 845	
acc att gtt tat cca atc aca tct gtt ccg ctt atc gcc tat tgt gtg	2770
Thr Ile Val Tyr Pro Ile Thr Ser Val Pro Leu Ile Ala Tyr Cys Val	
850 855 860	
ctt cct gct atc tgt ctt ctt acc aat aaa ttt atc att cct gag att	2818
Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile	
865 870 875 880	
agt aat tat gct gga atg ttc ttc att ctt ctt ttt gcc tcc att ttc	2866
Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser Ile Phe	
885 890 895	
gca act ggt ata ttg gag ctc aga tgg agt ggt gtt ggc att gaa gat	2914
Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp	
900 905 910	
tgg tgg aga aat gag cag ttt tgg gtt att ggt ggc acc tct gcc cat	2962
Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His	
915 920 925	
ctc ttc gcg gtg ttc cag ggt ctg ctg aaa gtg ttg gct ggg att gat	3010
Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp	
930 935 940	
acc aac ttc aca gtt acc tca aag gca tct gat gag gat ggc gac ttt	3058
Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp Phe	
945 950 955 960	
gct gag cta tat gtg ttc aag tgg acc agt ttg ctc atc cct ccg acc	3106
Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr	
965 970 975	
act gtt ctt gtc att aac ctg gtc gga atg gtg gca gga att tcg tat	3154
Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr	
980 985 990	

- 84 -

gcc att aac agc ggc tac caa tcc tgg ggt ccg ctc ttt gga aag ctg 3202
 Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu
 995 1000 1005

 ttc ttc tcg atc tgg gtg atc ctc cat ctc tac ccc ttc ctc aag ggt 3250
 Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly
 1010 1015 1020

 ctc atg ggc agg cag aac cgc acg cca aca atc gtc atc gtt tgg tcc 3298
 Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser
 1025 1030 1035 1040

 atc ctc ctt gcg tct atc ttc tcc ttg ctg tgg gtg aag atc gat cct 3346
 Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro
 1045 1050 1055

 ttc atc tcc ccg aca cag aaa gct gcc gcc ttg ggg caa tgt ggt gtg 3394
 Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys Gly Val
 1060 1065 1070

 aac t gctgatccag attgtgactc ttatctgaag aggctcagcc aaagatctgc 3448
 Asn

cccctcgtgt aaatacctga ggggggctaga tgggaatttt ttgttgtaga tgaggatgga 3508
 tctgcaccca agttatgcct ctgtttatta gcttcttcgg tgccgggtgct gctgcagaca 3568
 atcatggagc ctttctacct tgctttagt gctggccagc agcgtaaatt gtgaattctg 3628
 cattttttta tacgtggtgt ttattgtttt agagtaaatt atcatttgtt tgaggtaact 3688
 attcacacga actatatggc aatgctgtta tttaaaaa 3725

<210> 42
 <211> 1074
 <212> PRT
 <213> Zea mays

<400> 42
 Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 Phe Val Met Ile Arg His Asp Gly Asp Ala Pro Val Pro Ala Lys Pro
 20 25 30
 Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Thr Val
 35 40 45
 Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys Ala
 50 55 60
 Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly Asn
 65 70 75 80
 Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser
 85 90 95
 Pro Arg Val His Gly Asp Asp Glu Glu Glu Asp Val Asp Asp Leu Asp
 100 105 110
 Asn Glu Phe Asn Tyr Lys Gln Gly Asn Gly Lys Gly Pro Glu Trp Gln
 115 120 125
 Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Asp Pro
 130 135 140
 His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly Glu
 145 150 155 160
 Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr Ser

- 85 -

165 170 175
 Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp Pro
 180 185 190
 Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys Glu
 195 200 205
 Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Leu Gln Val
 210 215 220
 Thr Asn Lys Tyr Pro Glu Ala Arg Gly Asp Met Glu Gly Thr Gly Ser
 225 230 235 240
 Asn Gly Glu Asp Met Gln Met Val Asp Asp Ala Arg Leu Pro Leu Ser
 245 250 255
 Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg Ile Val
 260 265 270
 Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr Arg Ile
 275 280 285
 Ser His Pro Val Arg Asn Ala Tyr Gly Leu Trp Leu Val Ser Val Ile
 290 295 300
 Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe Pro Lys
 305 310 315 320
 Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu Arg
 325 330 335
 Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp Val Phe
 340 345 350
 Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala Asn
 355 360 365
 Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser
 370 375 380
 Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser Leu
 385 390 395 400
 Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys
 405 410 415
 His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln Lys Ile
 420 425 430
 Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg Arg
 435 440 445
 Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile Arg Ile Asn Ala Leu
 450 455 460
 Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Ala Asp
 465 470 475 480
 Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile
 485 490 495
 Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn Glu
 500 505 510
 Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln
 515 520 525
 His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala
 530 535 540
 Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His Tyr
 545 550 555 560
 Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met Asp
 565 570 575
 Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg Phe
 580 585 590
 Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val Phe
 595 600 605
 Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr
 610 615 620
 Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr Asp

- 86 -

625 630 635 640
 Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Val Lys Ser
 645 650 655
 Cys Cys Gly Arg Arg Lys Arg Lys Asn Lys Ser Tyr Met Asp Ser Gln
 660 665 670
 Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe Asn Met
 675 680 685
 Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg Ser Val
 690 695 700
 Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser Pro Ile
 705 710 715 720
 Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro Ser Thr
 725 730 735
 Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly
 740 745 750
 Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly
 755 760 765
 Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly
 770 775 780
 Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser
 785 790 795 800
 Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala
 805 810 815
 Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile Trp Tyr
 820 825 830
 Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr Ile Asn
 835 840 845
 Thr Ile Val Tyr Pro Ile Thr Ser Val Pro Leu Ile Ala Tyr Cys Val
 850 855 860
 Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile
 865 870 875 880
 Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser Ile Phe
 885 890 895
 Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp
 900 905 910
 Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His
 915 920 925
 Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp
 930 935 940
 Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp Phe
 945 950 955 960
 Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr
 965 970 975
 Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr
 980 985 990
 Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu
 995 1000 1005
 Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly
 1010 1015 1020
 Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser
 1025 1030 1035 1040
 Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro
 1045 1050 1055
 Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys Gly Val
 1060 1065 1070
 Asn Cys

- 87 -

<210> 43
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 43
 atggcgccca acaaggggat ggtgg
 25

<210> 44
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 44
 tcagcagttc acaccacatt gcccc
 25

<210> 45
 <211> 3813
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (215)...(3494)

<400> 45
 ccacagctca tataccaaga gccggagcag cttagcgcag cccagagcgg cgccgcgccca 60
 agcacaaccc ccaccgccca cagccgcgtg cgcattgtgag cggtcgccgc ggccgggaga 120
 ccagaggagg ggaggactac gtgcatttcg ctgtgccgcc gccgcgggggt tcgtgcgcga 180
 gcgagatccg gcgggggcggg gcgggggggcc tgag atg gag gct agc gcg ggg ctg 235
 Met Glu Ala Ser Ala Gly Leu
 1 5

gtg gcc ggc tcg cat aac cgg aac gag ctg gtg gtg atc cgc cgc gac 283
 Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg Arg Asp
 10 15 20

cgc gag tcg gga gcc gcg ggc ggc ggc gcg gcg cgc cgg gcg gag gcg 331
 Arg Glu Ser Gly Ala Ala Gly Gly Gly Ala Ala Arg Arg Ala Glu Ala
 25 30 35

ccg tgc cag ata tgc ggc gac gag gtc ggg gtg ggc ttc gac ggg gag 379
 Pro Cys Gln Ile Cys Gly Asp Glu Val Gly Val Gly Phe Asp Gly Glu
 40 45 50 55

ccc ttc gtg gcg tgc aac gag tgc gcc ttc ccc gtc tgc cgc gcc tgc 427
 Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Val Cys Arg Ala Cys
 60 65 70

tac gag tac gag cgc cgc gag ggc tcg caa gcg tgc ccg cag tgc agg 475
 Tyr Glu Tyr Glu Arg Arg Glu Gly Ser Gln Ala Cys Pro Gln Cys Arg
 75 80 85

acc cgc tac aag cgc ctc aag ggc tgc ccg cgg gtg gcc ggc gac gag 523
 Thr Arg Tyr Lys Arg Leu Lys Gly Cys Pro Arg Val Ala Gly Asp Glu
 90 95 100

- 88 -

gag gag gac ggc gtc gac gac ctg gag ggc gag ttc ggc ctg cag gac Glu Glu Asp Gly Val Asp Asp Leu Glu Gly Glu Phe Gly Leu Gln Asp 105 110 115	571
ggc gcc gcc cac gag gac gac ccg cag tac gtc gcc gag tcc atg ctc Gly Ala Ala His Glu Asp Asp Pro Gln Tyr Val Ala Glu Ser Met Leu 120 125 130 135	619
agg gcg cag atg agc tac ggc cgc ggc ggc gac gcg cac ccc ggc ttc Arg Ala Gln Met Ser Tyr Gly Arg Gly Gly Asp Ala His Pro Gly Phe 140 145 150	667
agc ccc gtc ccc aac gtg ccg ctc ctc acc aac ggc cag atg gtt gat Ser Pro Val Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp 155 160 165	715
gac atc ccg ccg gag cag cac gcg ctc gtg ccg tcc tac atg agc ggc Asp Ile Pro Pro Glu Gln His Ala Leu Val Pro Ser Tyr Met Ser Gly 170 175 180	763
ggc ggc ggc ggg ggc aag agg atc cac ccg ctc cct ttc gca gat ccc Gly Gly Gly Gly Gly Lys Arg Ile His Pro Leu Pro Phe Ala Asp Pro 185 190 195	811
aac ctt cca gtg caa ccg aga tcc atg gac ccg tcc aag gat ctg gcc Asn Leu Pro Val Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala 200 205 210 215	859
gcc tac gga tat ggc agc gtg gcc tgg aag gag aga atg gag ggc tgg Ala Tyr Gly Tyr Gly Ser Val Ala Trp Lys Glu Arg Met Glu Gly Trp 220 225 230	907
aag cag aag cag gag cgc ctg cag cat gtc agg agc gag ggt ggc ggt Lys Gln Lys Gln Glu Arg Leu Gln His Val Arg Ser Glu Gly Gly Gly 235 240 245	955
gat tgg gat ggc gac gat gca gat ctg cca cta atg gat gaa gct agg Asp Trp Asp Gly Asp Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg 250 255 260	1003
cag cca ttg tcc aga aaa gtc cct ata tca tca agc cga att aat ccc Gln Pro Leu Ser Arg Lys Val Pro Ile Ser Ser Ser Arg Ile Asn Pro 265 270 275	1051
tac agg atg att atc gtt atc cgg ttg gtg gtt ttg ggt ttc ttc ttc Tyr Arg Met Ile Ile Val Ile Arg Leu Val Val Leu Gly Phe Phe Phe 280 285 290 295	1099
cac tac cga gtg atg cat ccg gcg aaa gat gca ttt gca ttg tgg ctc His Tyr Arg Val Met His Pro Ala Lys Asp Ala Phe Ala Leu Trp Leu 300 305 310	1147
ata tct gta atc tgt gaa atc tgg ttt gcg atg tcc tgg att ctt gat Ile Ser Val Ile Cys Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp 315 320 325	1195
cag ttc cca aag tgg ctt cca atc gag aga gag act tac ctg gac cgt	1243

- 89 -

Gln Phe Pro Lys Trp Leu Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg	
330 335 340	
ttg tca cta agg ttt gac aag gaa ggt caa ccc tct cag ctt gct cca	1291
Leu Ser Leu Arg Phe Asp Lys Glu Gly Gln Pro Ser Gln Leu Ala Pro	
345 350 355	
atc gac ttc ttt gtc agt acg gtt gat ccc aca aag gaa cct ccc ttg	1339
Ile Asp Phe Phe Val Ser Thr Val Asp Pro Thr Lys Glu Pro Pro Leu	
360 365 370 375	
gtc aca gcg aac act gtc ctt tcc atc ctt tct gtg gat tat ccg gtt	1387
Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val	
380 385 390	
gag aag gtc tcc tgc tat gtt tct gat gat ggt gct gca atg ctt acg	1435
Glu Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr	
395 400 405	
ttt gaa gca ttg tct gaa aca tct gaa ttt gca aag aaa tgg gtt cct	1483
Phe Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro	
410 415 420	
ttc agc aaa aag ttt aat atc gag cct cgt gct cct gag tgg tac ttc	1531
Phe Ser Lys Lys Phe Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe	
425 430 435	
caa cag aag ata gac tac ctg aaa gac aag gtt gct gct tca ttt gtt	1579
Gln Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Ala Ala Ser Phe Val	
440 445 450 455	
agg gag agg agg gcg atg aag aga gaa tac gag gaa ttc aag gta agg	1627
Arg Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg	
460 465 470	
atc aat gcc ttg gtt gca aaa gcc caa aag gtt cct gag gaa gga tgg	1675
Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp	
475 480 485	
aca atg caa gat gga agc ccc tgg cct gga aac aac gta cgc gat cat	1723
Thr Met Gln Asp Gly Ser Pro Trp Pro Gly Asn Asn Val Arg Asp His	
490 495 500	
cct gga atg att cag gta ttc ctt ggc caa agt ggc ggt cgt gat gtg	1771
Pro Gly Met Ile Gln Val Phe Leu Gly Gln Ser Gly Gly Arg Asp Val	
505 510 515	
gaa gga aat gag ttg cct cgc ctg gtt tat gtc tcg aga gaa aag agg	1819
Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg	
520 525 530 535	
cca ggt tat aac cat cac aag aag gct ggt gcc atg aat gca ctg gtc	1867
Pro Gly Tyr Asn His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val	
540 545 550	
cgt gtc tct gct gtc tta tca aat gct gca tac cta ttg aac ttg gac	1915
Arg Val Ser Ala Val Leu Ser Asn Ala Ala Tyr Leu Leu Asn Leu Asp	
555 560 565	

- 90 -

tgt gat cac tac atc aac aat agc aag gcc ata aaa gag gct atg tgt Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys 570 575 580	1963
ttc atg atg gat cct ttg gtg ggg aag aaa gtg tgc tat gta cag ttc Phe Met Met Asp Pro Leu Val Gly Lys Lys Val Cys Tyr Val Gln Phe 585 590 595	2011
cct cag agg ttt gat ggt att gac aaa aat gat cga tac gct aac agg Pro Gln Arg Phe Asp Gly Ile Asp Lys Asn Asp Arg Tyr Ala Asn Arg 600 605 610 615	2059
aac gtt gtc ttt ttt gac atc aac atg aaa ggt ttg gac ggt att caa Asn Val Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln 620 625 630	2107
gga ccc att tat gtg ggt act gga tgt gtt ttc aga cgg cag gca ctg Gly Pro Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu 635 640 645	2155
tat ggt tat gat gct cct aaa acg aag aag cca cca tca aga act tgc Tyr Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro Pro Ser Arg Thr Cys 650 655 660	2203
aac tgc tgg ccc aag tgg tgc ctc tct tgc tgc tgc agc agg aac aag Asn Cys Trp Pro Lys Trp Cys Leu Ser Cys Cys Cys Ser Arg Asn Lys 665 670 675	2251
aat aaa aag aag act aca aaa cca aag acg gag aag aag aaa aga tta Asn Lys Lys Lys Thr Thr Lys Lys Pro Lys Thr Glu Lys Lys Lys Arg Leu 680 685 690 695	2299
ttt ttc aag aaa gca gaa aac cca tct cct gca tat gct ttg ggt gaa Phe Phe Lys Lys Ala Glu Asn Pro Ser Pro Ala Tyr Ala Leu Gly Glu 700 705 710	2347
att gat gaa ggt gct cca ggt gct gat atc gag aag gcc gga atc gta Ile Asp Glu Gly Ala Pro Gly Ala Asp Ile Glu Lys Ala Gly Ile Val 715 720 725	2395
aat caa cag aaa cta gag aag aaa ttt ggg cag tct tct gtt ttt gtc Asn Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln Ser Ser Val Phe Val 730 735 740	2443
gca tca aca ctt ctt gag aac gga ggg acc ctg aag agc gca agt cca Ala Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu Lys Ser Ala Ser Pro 745 750 755	2491
gct tct ctt ctg aag gaa gct ata cat gtt atc agc tgc ggc tac gaa Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu 760 765 770 775	2539
gac aag acc gac tgg gga aaa gag att ggc tgg att tac gga tcg atc Asp Lys Thr Asp Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly Ser Ile 780 785 790	2587
aca gag gat atc ttg act gga ttt aag atg cac tgc cat ggc tgg cgg	2635

- 91 -

Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys His Gly Trp Arg	
795 800 805	
tct att tac tgc atc ccg aag cgg cct gca ttc aaa ggt tct gcg cct	2683
Ser Ile Tyr Cys Ile Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro	
810 815 820	
ctg aac ctt tcc gac cgt ctt cac cag gtc ctt cgc tgg gcc ctt ggg	2731
Leu Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly	
825 830 835	
tcc gtc gaa att ttc ttc agc aag cac tgc cca ctt tgg tac gga tac	2779
Ser Val Glu Ile Phe Phe Ser Lys His Cys Pro Leu Trp Tyr Gly Tyr	
840 845 850 855	
ggc ggc ggg cta aaa ttc ctg gaa agg ttt tct tat atc aac tcc atc	2827
Gly Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser Tyr Ile Asn Ser Ile	
860 865 870	
gtt tat ccc tgg acg tcc att cct ctc ctg gct tac tgt acc ttg cct	2875
Val Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Leu Pro	
875 880 885	
gcc atc tgc ctg ctc acg ggg aag ttt atc aca cca gag ctt acc aat	2923
Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr Pro Glu Leu Thr Asn	
890 895 900	
gtc gcc agt atc tgg ttc atg gca ctt ttc atc tgc atc tcc gtg acc	2971
Val Ala Ser Ile Trp Phe Met Ala Leu Phe Ile Cys Ile Ser Val Thr	
905 910 915	
ggc atc ctg gaa atg agg tgg agt ggc gtg gcc atc gac gac tgg tgg	3019
Gly Ile Leu Glu Met Arg Trp Ser Gly Val Ala Ile Asp Asp Trp Trp	
920 925 930 935	
agg aac gag cag ttc tgg gtc atc gga ggc gtt tcg gcg cat ctg ttc	3067
Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe	
940 945 950	
gcg gtg ttc cag ggc ctg ctg aag gtg ttc gcc ggc atc gac acg agc	3115
Ala Val Phe Gln Gly Leu Leu Lys Val Phe Ala Gly Ile Asp Thr Ser	
955 960 965	
ttc acc gtg acg tcg aag gcc ggg gac gac gag gag ttc tcg gag ctg	3163
Phe Thr Val Thr Ser Lys Ala Gly Asp Asp Glu Glu Phe Ser Glu Leu	
970 975 980	
tac acg ttc aag tgg acc acc ctg ctg ata ccc ccg acc acg ctc ctc	3211
Tyr Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu	
985 990 995	
ctg ctg aac ttc atc ggg gtg gtg gcc ggg atc tcg aac gcg atc aac	3259
Leu Leu Asn Phe Ile Gly Val Val Ala Gly Ile Ser Asn Ala Ile Asn	
1000 1005 1010 1015	
aac ggg tac gag tcg tgg ggc ccc ctg ttc ggg aag ctc ttc ttc gcc	3307
Asn Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala	
1020 1025 1030	

- 92 -

ttc tgg gtg atc gtc cac ctg tac ccg ttc ctc aag ggt ctg gtg ggg 3355
 Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Val Gly
 1035 1040 1045
 agg cag aac agg acg ccg acg atc gtc atc gtc tgg tcc atc ctg ctg 3403
 Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu Leu
 1050 1055 1060
 gcc tcg atc ttc tcg ctc ctg tgg gtc cgc gtc gac ccg ttc ctc gcc 3451
 Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Val Asp Pro Phe Leu Ala
 1065 1070 1075
 aag agc aac ggc ccg ctc ctg gag gag tgt ggc ctg gac tgc a 3494
 Lys Ser Asn Gly Pro Leu Leu Glu Glu Cys Gly Leu Asp Cys
 1080 1085 1090
 actgaagtgg gggccccctg tcactogaag ttctgtcacg ggcgaattac gcctgatttt 3554
 ttgttgttgt tgttgttgga attctttgct gtagatagaa accacatgtc cacggcatct 3614
 ctgctgtgtc cattggagca ggagagaggt gcctgctgct gtttgttgag taaattaaaa 3674
 gttttaaagt tatacagtga tgcacattcc agtgcccagt gtattccctt ttacagtct 3734
 gtatattagc gacaaaggac atattgggta ggagtttgat tcttttgtaa aaaaaaaaaa 3794
 aaaaaaaaaa aaaaaaaaaa 3813

<210> 46
 <211> 1094
 <212> PRT
 <213> Zea mays

<400> 46

Met Glu Ala Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu
 1 5 10 15
 Leu Val Val Ile Arg Arg Asp Arg Glu Ser Gly Ala Ala Gly Gly Gly
 20 25 30
 Ala Ala Arg Arg Ala Glu Ala Pro Cys Gln Ile Cys Gly Asp Glu Val
 35 40 45
 Gly Val Gly Phe Asp Gly Glu Pro Phe Val Ala Cys Asn Glu Cys Ala
 50 55 60
 Phe Pro Val Cys Arg Ala Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Ser
 65 70 75 80
 Gln Ala Cys Pro Gln Cys Arg Thr Arg Tyr Lys Arg Leu Lys Gly Cys
 85 90 95
 Pro Arg Val Ala Gly Asp Glu Glu Glu Asp Gly Val Asp Asp Leu Glu
 100 105 110
 Gly Glu Phe Gly Leu Gln Asp Gly Ala Ala His Glu Asp Asp Pro Gln
 115 120 125
 Tyr Val Ala Glu Ser Met Leu Arg Ala Gln Met Ser Tyr Gly Arg Gly
 130 135 140
 Gly Asp Ala His Pro Gly Phe Ser Pro Val Pro Asn Val Pro Leu Leu
 145 150 155 160
 Thr Asn Gly Gln Met Val Asp Asp Ile Pro Pro Glu Gln His Ala Leu
 165 170 175
 Val Pro Ser Tyr Met Ser Gly Gly Gly Gly Gly Lys Arg Ile His
 180 185 190
 Pro Leu Pro Phe Ala Asp Pro Asn Leu Pro Val Gln Pro Arg Ser Met
 195 200 205
 Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr Gly Ser Val Ala Trp
 210 215 220

- 93 -

Lys Glu Arg Met Glu Gly Trp Lys Gln Lys Gln Glu Arg Leu Gln His
 225 230 235 240
 Val Arg Ser Glu Gly Gly Gly Asp Trp Asp Gly Asp Asp Ala Asp Leu
 245 250 255
 Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg Lys Val Pro Ile
 260 265 270
 Ser Ser Ser Arg Ile Asn Pro Tyr Arg Met Ile Ile Val Ile Arg Leu
 275 280 285
 Val Val Leu Gly Phe Phe Phe His Tyr Arg Val Met His Pro Ala Lys
 290 295 300
 Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys Glu Ile Trp Phe
 305 310 315 320
 Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Leu Pro Ile Glu
 325 330 335
 Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe Asp Lys Glu Gly
 340 345 350
 Gln Pro Ser Gln Leu Ala Pro Ile Asp Phe Phe Val Ser Thr Val Asp
 355 360 365
 Pro Thr Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val Leu Ser Ile
 370 375 380
 Leu Ser Val Asp Tyr Pro Val Glu Lys Val Ser Cys Tyr Val Ser Asp
 385 390 395 400
 Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser Glu Thr Ser Glu
 405 410 415
 Phe Ala Lys Lys Trp Val Pro Phe Ser Lys Lys Phe Asn Ile Glu Pro
 420 425 430
 Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp Tyr Leu Lys Asp
 435 440 445
 Lys Val Ala Ala Ser Phe Val Arg Glu Arg Arg Ala Met Lys Arg Glu
 450 455 460
 Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln
 465 470 475 480
 Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly Ser Pro Trp Pro
 485 490 495
 Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln Val Phe Leu Gly
 500 505 510
 Gln Ser Gly Gly Arg Asp Val Glu Gly Asn Glu Leu Pro Arg Leu Val
 515 520 525
 Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His His Lys Lys Ala
 530 535 540
 Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Ser Asn Ala
 545 550 555 560
 Ala Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys
 565 570 575
 Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro Leu Val Gly Lys
 580 585 590
 Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Lys
 595 600 605
 Asn Asp Arg Tyr Ala Asn Arg Asn Val Val Phe Phe Asp Ile Asn Met
 610 615 620
 Lys Gly Leu Asp Gly Ile Gln Gly Pro Ile Tyr Val Gly Thr Gly Cys
 625 630 635 640
 Val Phe Arg Arg Gln Ala Leu Tyr Gly Tyr Asp Ala Pro Lys Thr Lys
 645 650 655
 Lys Pro Pro Ser Arg Thr Cys Asn Cys Trp Pro Lys Trp Cys Leu Ser
 660 665 670
 Cys Cys Cys Ser Arg Asn Lys Asn Lys Lys Lys Thr Thr Lys Pro Lys
 675 680 685

- 94 -

```

Thr Glu Lys Lys Lys Arg Leu Phe Phe Lys Lys Ala Glu Asn Pro Ser
  690                      695                      700
Pro Ala Tyr Ala Leu Gly Glu Ile Asp Glu Gly Ala Pro Gly Ala Asp
705                      710                      715                      720
Ile Glu Lys Ala Gly Ile Val Asn Gln Gln Lys Leu Glu Lys Lys Phe
                      725                      730                      735
Gly Gln Ser Ser Val Phe Val Ala Ser Thr Leu Leu Glu Asn Gly Gly
                      740                      745                      750
Thr Leu Lys Ser Ala Ser Pro Ala Ser Leu Leu Lys Glu Ala Ile His
                      755                      760                      765
Val Ile Ser Cys Gly Tyr Glu Asp Lys Thr Asp Trp Gly Lys Glu Ile
770                      775                      780
Gly Trp Ile Tyr Gly Ser Ile Thr Glu Asp Ile Leu Thr Gly Phe Lys
785                      790                      795                      800
Met His Cys His Gly Trp Arg Ser Ile Tyr Cys Ile Pro Lys Arg Pro
                      805                      810                      815
Ala Phe Lys Gly Ser Ala Pro Leu Asn Leu Ser Asp Arg Leu His Gln
                      820                      825                      830
Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Phe Phe Ser Lys His
                      835                      840                      845
Cys Pro Leu Trp Tyr Gly Tyr Gly Gly Gly Leu Lys Phe Leu Glu Arg
850                      855                      860
Phe Ser Tyr Ile Asn Ser Ile Val Tyr Pro Trp Thr Ser Ile Pro Leu
865                      870                      875                      880
Leu Ala Tyr Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe
                      885                      890                      895
Ile Thr Pro Glu Leu Thr Asn Val Ala Ser Ile Trp Phe Met Ala Leu
900                      905                      910
Phe Ile Cys Ile Ser Val Thr Gly Ile Leu Glu Met Arg Trp Ser Gly
915                      920                      925
Val Ala Ile Asp Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly
930                      935                      940
Gly Val Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val
945                      950                      955                      960
Phe Ala Gly Ile Asp Thr Ser Phe Thr Val Thr Ser Lys Ala Gly Asp
                      965                      970                      975
Asp Glu Glu Phe Ser Glu Leu Tyr Thr Phe Lys Trp Thr Thr Leu Leu
980                      985                      990
Ile Pro Pro Thr Thr Leu Leu Leu Leu Asn Phe Ile Gly Val Val Ala
995                      1000                      1005
Gly Ile Ser Asn Ala Ile Asn Asn Gly Tyr Glu Ser Trp Gly Pro Leu
1010                      1015                      1020
Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr Pro
1025                      1030                      1035                      1040
Phe Leu Lys Gly Leu Val Gly Arg Gln Asn Arg Thr Pro Thr Ile Val
                      1045                      1050                      1055
Ile Val Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val
1060                      1065                      1070
Arg Val Asp Pro Phe Leu Ala Lys Ser Asn Gly Pro Leu Leu Glu Glu
1075                      1080                      1085
Cys Gly Leu Asp Cys Asn
1090

```

<210> 47

<211> 25

<212> DNA

<213> Zea mays

- 95 -

<400> 47
atggaggcta gcgcggggct ggtgg
25

<210> 48
<211> 25
<212> DNA
<213> Zea mays

<400> 48
tcagttgcag tccaggccac actcc
25

<210> 49
<211> 3746
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (321) ... (3449)

<400> 49
ctaggatcaa aaccgtctcg ccgctgcaat aatcttttgt caattcttaa tccctcgcgt 60
cgacagcgac agcggaaacca actcacgttg ccgcggcttc ctccatcggg gcggtgccct 120
gtccttttct ctcgtccctc ctccccccgt atagttaagc ccgcgcccg c tactactact 180
actagcagca gcagcgtct cgcagcggga gatgcggtgt tgatccgtgc cccgctcgga 240
tctcgggact ggtgccggct ctgccaggc cccaggtcc aggccagctc cctcgacgtt 300
tctcggcgag ctcgcttgcc atg gag ggc gac gcg gac ggc gtg aag tcg ggg 353
Met Glu Gly Asp Ala Asp Gly Val Lys Ser Gly
1 5 10
agg cgc ggt ggc gga cag gtg tgc cag atc tgc ggc gac ggc gtg ggc 401
Arg Arg Gly Gly Gly Gln Val Cys Gln Ile Cys Gly Asp Gly Val Gly
15 20 25
acc acg gcg gag ggg gac gtc ttc gcc gcc tgc gac gtc tgc ggg ttt 449
Thr Thr Ala Glu Gly Asp Val Phe Ala Ala Cys Asp Val Cys Gly Phe
30 35 40
ccg gtg tgc cgc ccc tgc tac gag tac gag cgc aag gac ggc acg cag 497
Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Thr Gln
45 50 55
gcg tgc ccc cag tgc aag acc aag tac aag cgc cac aag ggg agc ccg 545
Ala Cys Pro Gln Cys Lys Thr Lys Tyr Lys Arg His Lys Gly Ser Pro
60 65 70 75
gcg atc cgt ggg gag gaa gga gac gac act gat gcc gat agc gac ttc 593
Ala Ile Arg Gly Glu Glu Gly Asp Asp Thr Asp Ala Asp Ser Asp Phe
80 85 90
aat tac ctt gca tct ggc aat gag gac cag aag cag aag att gcc gac 641
Asn Tyr Leu Ala Ser Gly Asn Glu Asp Gln Lys Gln Lys Ile Ala Asp
95 100 105
aga atg cgc agc tgg cgc atg aac gtt ggg ggc agc ggg gat gtt ggt 689
Arg Met Arg Ser Trp Arg Met Asn Val Gly Gly Ser Gly Asp Val Gly

- 96 -

110	115	120	
cgc ccc aag tat gac agt ggc gag atc ggg ctt acc aag tat gac agt			737
Arg Pro Lys Tyr Asp Ser Gly Glu Ile Gly Leu Thr Lys Tyr Asp Ser			
125	130	135	
ggc gag att cct cgg gga tac atc cca tca gtc act aac agc cag atc			785
Gly Glu Ile Pro Arg Gly Tyr Ile Pro Ser Val Thr Asn Ser Gln Ile			
140	145	150	155
tca gga gaa atc cct ggt gct tcc cct gac cat cat atg atg tcc cca			833
Ser Gly Glu Ile Pro Gly Ala Ser Pro Asp His His Met Met Ser Pro			
160	165	170	
act ggg aac att ggc aag cgt gct cca ttt ccc tat gtg aac cat tcg			881
Thr Gly Asn Ile Gly Lys Arg Ala Pro Phe Pro Tyr Val Asn His Ser			
175	180	185	
cca aat ccg tca agg gag ttc tct ggt agc att ggg aat gtt gcc tgg			929
Pro Asn Pro Ser Arg Glu Phe Ser Gly Ser Ile Gly Asn Val Ala Trp			
190	195	200	
aaa gag agg gtt gat ggc tgg aaa atg aag cag gac aag ggg acg att			977
Lys Glu Arg Val Asp Gly Trp Lys Met Lys Gln Asp Lys Gly Thr Ile			
205	210	215	
ccc atg acg aat ggc aca agc att gct ccc tct gag ggt cgg ggt gtt			1025
Pro Met Thr Asn Gly Thr Ser Ile Ala Pro Ser Glu Gly Arg Gly Val			
220	225	230	235
ggg gat att gat gca tca act gat tac aac atg gaa gat gcc tta ttg			1073
Gly Asp Ile Asp Ala Ser Thr Asp Tyr Asn Met Glu Asp Ala Leu Leu			
240	245	250	
aac gac gaa act cga cag cct cta tct agg aaa gtt cca ctt cct tcc			1121
Asn Asp Glu Thr Arg Gln Pro Leu Ser Arg Lys Val Pro Leu Pro Ser			
255	260	265	
tcc agg ata aat cca tac agg atg gtc att gtg ctg cga ttg att gtt			1169
Ser Arg Ile Asn Pro Tyr Arg Met Val Ile Val Leu Arg Leu Ile Val			
270	275	280	
cta agc atc ttc ttg cac tac cgt atc aca aat cct gtg cgc aat gca			1217
Leu Ser Ile Phe Leu His Tyr Arg Ile Thr Asn Pro Val Arg Asn Ala			
285	290	295	
tac cca tta tgg ctt cta tct gtt ata tgt gag atc tgg ttt gct ctt			1265
Tyr Pro Leu Trp Leu Leu Ser Val Ile Cys Glu Ile Trp Phe Ala Leu			
300	305	310	315
tcg tgg ata ttg gat cag ttc cct aag tgg ttt cca atc aac cgg gag			1313
Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Phe Pro Ile Asn Arg Glu			
320	325	330	
acg tac ctt gat agg ctg gca tta agg tat gac cgg gaa ggt gag cca			1361
Thr Tyr Leu Asp Arg Leu Ala Leu Arg Tyr Asp Arg Glu Gly Glu Pro			
335	340	345	

- 97 -

tct cag ttg gct gct gtt gac att ttc gtc agt aca gtc gac cca atg	1409
Ser Gln Leu Ala Ala Val Asp Ile Phe Val Ser Thr Val Asp Pro Met	
350 355 360	
aag gag cct cct ctt gtc act gcc aat acc gtg cta tcc att ctt gct	1457
Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ala	
365 370 375	
gtg gat tac cct gtg gat aag gtc tct tgc tat gta tct gat gat gga	1505
Val Asp Tyr Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly	
380 385 390 395	
gct gcg atg ctg aca ttt gat gca cta gct gag act tca gag ttt gct	1553
Ala Ala Met Leu Thr Phe Asp Ala Leu Ala Glu Thr Ser Glu Phe Ala	
400 405 410	
aga aaa tgg gta cca ttt gtt aag aag tac aac att gaa cct aga gct	1601
Arg Lys Trp Val Pro Phe Val Lys Lys Tyr Asn Ile Glu Pro Arg Ala	
415 420 425	
cct gaa tgg tac ttc tcc cag aaa att gat tac ttg aag gac aaa gtg	1649
Pro Glu Trp Tyr Phe Ser Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val	
430 435 440	
cac cct tca ttt gtt aaa gac cgc cgg gcc atg aag aga gaa tat gaa	1697
His Pro Ser Phe Val Lys Asp Arg Arg Ala Met Lys Arg Glu Tyr Glu	
445 450 455	
gaa ttc aaa gtt agg gta aat ggc ctt gtt gct aag gca cag aaa gtt	1745
Glu Phe Lys Val Arg Val Asn Gly Leu Val Ala Lys Ala Gln Lys Val	
460 465 470 475	
cct gag gaa gga tgg atc atg caa gat ggc aca cca tgg cca gga aac	1793
Pro Glu Glu Gly Trp Ile Met Gln Asp Gly Thr Pro Trp Pro Gly Asn	
480 485 490	
aat acc mgg gac cat cct gga atg att cag gtt ttc ctt ggt cac agt	1841
Asn Thr Xaa Asp His Pro Gly Met Ile Gln Val Phe Leu Gly His Ser	
495 500 505	
ggt ggc ctt gat act gag ggc aat gag cta ccc cgt ttg gtc tat gtt	1889
Gly Gly Leu Asp Thr Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val	
510 515 520	
tct cgt gaa aag cgt cct gga ttc cag cat cac aag aaa gct ggt gcc	1937
Ser Arg Glu Lys Arg Pro Gly Phe Gln His His Lys Lys Ala Gly Ala	
525 530 535	
atg aat gct ctt gtt cgt gtc tca gct gtg ctt acc aat gga caa tac	1985
Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Gly Gln Tyr	
540 545 550 555	
atg ttg aat ctt gat tgt gat cac tac att aac aac agt aag gct ctc	2033
Met Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Leu	
560 565 570	
agg gaa gct atg tgc ttc ctt atg gac cct aac cta gga agg agt gtc	2081
Arg Glu Ala Met Cys Phe Leu Met Asp Pro Asn Leu Gly Arg Ser Val	

- 98 -

575	580	585	
tgc tac gtc cag ttt ccc cag aga ttc gat ggc att gac agg aat gat Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp 590 595 600			2129
cga tat gcc aac agg aac acc gtg ttt ttc gat att aac ttg aga ggt Arg Tyr Ala Asn Arg Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly 605 610 615			2177
ctt gat ggc atc caa gga cca gtt tat gtc gga act ggc tgt gtt ttc Leu Asp Gly Ile Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe 620 625 630 635			2225
aac cga aca gct cta tat ggt tat gag ccc cca att aag cag aag aag Asn Arg Thr Ala Leu Tyr Gly Tyr Glu Pro Pro Ile Lys Gln Lys Lys 640 645 650			2273
ggt ggt ttc ttg tca tca cta tgt ggc ggt agg aag aag gca agc aaa Gly Gly Phe Leu Ser Ser Leu Cys Gly Gly Arg Lys Lys Ala Ser Lys 655 660 665			2321
tca aag aag ggc tcg gac aag aag aag tcg cag aag cat gtg gac agt Ser Lys Lys Gly Ser Asp Lys Lys Lys Ser Gln Lys His Val Asp Ser 670 675 680			2369
tct gtg cca gta ttc aac ctt gaa gat ata gag gag gga gtt gaa ggc Ser Val Pro Val Phe Asn Leu Glu Asp Ile Glu Glu Gly Val Glu Gly 685 690 695			2417
gct gga ttt gac gac gag aaa tca ctt ctt atg tct caa atg agc ctg Ala Gly Phe Asp Asp Glu Lys Ser Leu Leu Met Ser Gln Met Ser Leu 700 705 710 715			2465
gag aag aga ttt ggc cag tcc gca gcg ttt gtt gcc tcc act ctg atg Glu Lys Arg Phe Gly Gln Ser Ala Ala Phe Val Ala Ser Thr Leu Met 720 725 730			2513
gag tat ggt ggt gtt cct cag tcc gca act ccg gag tct ctt ctg aaa Glu Tyr Gly Gly Val Pro Gln Ser Ala Thr Pro Glu Ser Leu Leu Lys 735 740 745			2561
gaa gct atc cat gtt ata agc tgt ggc tat gag gac aag act gaa tgg Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp 750 755 760			2609
gga act gag atc ggg tgg atc tac ggt tct gtg aca gaa gac att ctc Gly Thr Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu 765 770 775			2657
acc gga ttc aag atg cac gcg cga ggc tgg cgg tcg atc tac tgc atg Thr Gly Phe Lys Met His Ala Arg Gly Trp Arg Ser Ile Tyr Cys Met 780 785 790 795			2705
ccc aag cgg cca gct ttc aag ggg tct gcc ccc atc aat ctt tcg gac Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp 800 805 810			2753

- 99 -

cgt ctg aac cag gtg ctc cgg tgg gct ctt ggg tcc gtg gag atc ctc	2801
Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu	
815 820 825	
ttc agc cgg cac tgc ccc ctg tgg tac ggc tac gga ggg cgg ctc aag	2849
Phe Ser Arg His Cys Pro Leu Trp Tyr Gly Tyr Gly Gly Arg Leu Lys	
830 835 840	
ttc ctg gag aga ttc gcg tac atc aac acc acc atc tac ccg ctc acg	2897
Phe Leu Glu Arg Phe Ala Tyr Ile Asn Thr Thr Ile Tyr Pro Leu Thr	
845 850 855	
tcc atc ccg ctt ctc atc tac tgc atc ctg ccc gcc atc tgt ctg ctc	2945
Ser Ile Pro Leu Leu Ile Tyr Cys Ile Leu Pro Ala Ile Cys Leu Leu	
860 865 870 875	
acc gga aag ttc atc att cca gag atc agc aac ttc gcc agc atc tgg	2993
Thr Gly Lys Phe Ile Ile Pro Glu Ile Ser Asn Phe Ala Ser Ile Trp	
880 885 890	
ttc atc tcc ctc ttc atc tcg atc ttc gcc acg ggc atc ctg gag atg	3041
Phe Ile Ser Leu Phe Ile Ser Ile Phe Ala Thr Gly Ile Leu Glu Met	
895 900 905	
agg tgg agc ggg gtg ggc atc gac gag tgg tgg agg aac gag cag ttc	3089
Arg Trp Ser Gly Val Gly Ile Asp Glu Trp Trp Arg Asn Glu Gln Phe	
910 915 920	
tgg gtg atc ggg ggc atc tcc gcg cac ctc ttc gcc gtg ttc cag ggc	3137
Trp Val Ile Gly Gly Ile Ser Ala His Leu Phe Ala Val Phe Gln Gly	
925 930 935	
ctg ctc aag gtg ctg gcc ggc atc gac acc aac ttc acc gtc acc tcc	3185
Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser	
940 945 950 955	
aag gcc tcg gac gag gac ggc gac ttc gcg gag ctg tac atg ttc aag	3233
Lys Ala Ser Asp Glu Asp Gly Asp Phe Ala Glu Leu Tyr Met Phe Lys	
960 965 970	
tgg acg acg ctc ctg atc ccg ccc acc acc atc ctg atc atc aac ctg	3281
Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Ile Leu Ile Ile Asn Leu	
975 980 985	
gtc ggc gtc gtc gcc ggc atc tcc tac gcc atc aac agc gga tac cag	3329
Val Gly Val Val Ala Gly Ile Ser Tyr Ala Ile Asn Ser Gly Tyr Gln	
990 995 1000	
tcg tgg ggc ccg ctc ttc ggc aag ctc ttc ttc gcc ttc tgg gtc atc	3377
Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile	
1005 1010 1015	
gtc cac ctg tac ccg ttc ctc aag ggc ctc atg ggc agg cag aac cgc	3425
Val His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg	
1020 1025 1030 1035	
acc ccg acc atc gtc gtc gtc tgg gccatccctgc tggcgtccat cttctccttg	3479
Thr Pro Thr Ile Val Val Val Trp	

- 100 -

1040

```

ctgtgggttc gcatcgaccc cttcaccacc cgcgtcactg gcccggtatac ccagacgtgt 3539
ggcatcaact gctaggggaag tggaagggtt gtactttgta gaaacggagg aataccacgt 3599
gccatctgtt gtctgttaag ttatatatat ataagcagca agtggcggtta ttacagcta 3659
cgtacagacc agtggatatt gtttaccaca aagttttact tgtgttaata tgcattcttt 3719
tggtgatata aaaaaaaaaa aaaaaaa 3746

```

```

<210> 50
<211> 1043
<212> PRT
<213> Zea mays

```

```

<400> 50
Met Glu Gly Asp Ala Asp Gly Val Lys Ser Gly Arg Arg Gly Gly Gly
 1      5      10      15
Gln Val Cys Gln Ile Cys Gly Asp Gly Val Gly Thr Thr Ala Glu Gly
 20      25      30
Asp Val Phe Ala Ala Cys Asp Val Cys Gly Phe Pro Val Cys Arg Pro
 35      40      45
Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Thr Gln Ala Cys Pro Gln Cys
 50      55      60
Lys Thr Lys Tyr Lys Arg His Lys Gly Ser Pro Ala Ile Arg Gly Glu
 65      70      75      80
Glu Gly Asp Asp Thr Asp Ala Asp Ser Asp Phe Asn Tyr Leu Ala Ser
 85      90      95
Gly Asn Glu Asp Gln Lys Gln Lys Ile Ala Asp Arg Met Arg Ser Trp
100      105      110
Arg Met Asn Val Gly Gly Ser Gly Asp Val Gly Arg Pro Lys Tyr Asp
115      120      125
Ser Gly Glu Ile Gly Leu Thr Lys Tyr Asp Ser Gly Glu Ile Pro Arg
130      135      140
Gly Tyr Ile Pro Ser Val Thr Asn Ser Gln Ile Ser Gly Glu Ile Pro
145      150      155      160
Gly Ala Ser Pro Asp His His Met Met Ser Pro Thr Gly Asn Ile Gly
165      170      175
Lys Arg Ala Pro Phe Pro Tyr Val Asn His Ser Pro Asn Pro Ser Arg
180      185      190
Glu Phe Ser Gly Ser Ile Gly Asn Val Ala Trp Lys Glu Arg Val Asp
195      200      205
Gly Trp Lys Met Lys Gln Asp Lys Gly Thr Ile Pro Met Thr Asn Gly
210      215      220
Thr Ser Ile Ala Pro Ser Glu Gly Arg Gly Val Gly Asp Ile Asp Ala
225      230      235      240
Ser Thr Asp Tyr Asn Met Glu Asp Ala Leu Leu Asn Asp Glu Thr Arg
245      250      255
Gln Pro Leu Ser Arg Lys Val Pro Leu Pro Ser Ser Arg Ile Asn Pro
260      265      270
Tyr Arg Met Val Ile Val Leu Arg Leu Ile Val Leu Ser Ile Phe Leu
275      280      285
His Tyr Arg Ile Thr Asn Pro Val Arg Asn Ala Tyr Pro Leu Trp Leu
290      295      300
Leu Ser Val Ile Cys Glu Ile Trp Phe Ala Leu Ser Trp Ile Leu Asp
305      310      315      320
Gln Phe Pro Lys Trp Phe Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg
325      330      335
Leu Ala Leu Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Ala
340      345      350

```

- 101 -

Val Asp Ile Phe Val Ser Thr Val Asp Pro Met Lys Glu Pro Pro Leu
 355 360 365
 Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val
 370 375 380
 Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr
 385 390 395 400
 Phe Asp Ala Leu Ala Glu Thr Ser Glu Phe Ala Arg Lys Trp Val Pro
 405 410 415
 Phe Val Lys Lys Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe
 420 425 430
 Ser Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val His Pro Ser Phe Val
 435 440 445
 Lys Asp Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg
 450 455 460
 Val Asn Gly Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp
 465 470 475 480
 Ile Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Thr Xaa Asp His
 485 490 495
 Pro Gly Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr
 500 505 510
 Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg
 515 520 525
 Pro Gly Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val
 530 535 540
 Arg Val Ser Ala Val Leu Thr Asn Gly Gln Tyr Met Leu Asn Leu Asp
 545 550 555 560
 Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Leu Arg Glu Ala Met Cys
 565 570 575
 Phe Leu Met Asp Pro Asn Leu Gly Arg Ser Val Cys Tyr Val Gln Phe
 580 585 590
 Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp Arg Tyr Ala Asn Arg
 595 600 605
 Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly Leu Asp Gly Ile Gln
 610 615 620
 Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe Asn Arg Thr Ala Leu
 625 630 635 640
 Tyr Gly Tyr Glu Pro Pro Ile Lys Gln Lys Lys Gly Gly Phe Leu Ser
 645 650 655
 Ser Leu Cys Gly Gly Arg Lys Lys Ala Ser Lys Ser Lys Lys Gly Ser
 660 665 670
 Asp Lys Lys Lys Ser Gln Lys His Val Asp Ser Ser Val Pro Val Phe
 675 680 685
 Asn Leu Glu Asp Ile Glu Glu Gly Val Glu Gly Ala Gly Phe Asp Asp
 690 695 700
 Glu Lys Ser Leu Leu Met Ser Gln Met Ser Leu Glu Lys Arg Phe Gly
 705 710 715 720
 Gln Ser Ala Ala Phe Val Ala Ser Thr Leu Met Glu Tyr Gly Gly Val
 725 730 735
 Pro Gln Ser Ala Thr Pro Glu Ser Leu Leu Lys Glu Ala Ile His Val
 740 745 750
 Ile Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Thr Glu Ile Gly
 755 760 765
 Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met
 770 775 780
 His Ala Arg Gly Trp Arg Ser Ile Tyr Cys Met Pro Lys Arg Pro Ala
 785 790 795 800
 Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val
 805 810 815

- 102 -

Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu Phe Ser Arg His Cys
 820 825 830
 Pro Leu Trp Tyr Gly Tyr Gly Gly Arg Leu Lys Phe Leu Glu Arg Phe
 835 840 845
 Ala Tyr Ile Asn Thr Thr Ile Tyr Pro Leu Thr Ser Ile Pro Leu Leu
 850 855 860
 Ile Tyr Cys Ile Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile
 865 870 875 880
 Ile Pro Glu Ile Ser Asn Phe Ala Ser Ile Trp Phe Ile Ser Leu Phe
 885 890 895
 Ile Ser Ile Phe Ala Thr Gly Ile Leu Glu Met Arg Trp Ser Gly Val
 900 905 910
 Gly Ile Asp Glu Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly
 915 920 925
 Ile Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu
 930 935 940
 Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu
 945 950 955 960
 Asp Gly Asp Phe Ala Glu Leu Tyr Met Phe Lys Trp Thr Thr Leu Leu
 965 970 975
 Ile Pro Pro Thr Thr Ile Leu Ile Ile Asn Leu Val Gly Val Val Ala
 980 985 990
 Gly Ile Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu
 995 1000 1005
 Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val His Leu Tyr Pro
 1010 1015 1020
 Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val
 1025 1030 1035 1040
 Val Val Trp

<210> 51
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 51
 atggagggcg acgcggacgg cgtga
 25

<210> 52
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 52
 ctagcagttg atgccacacg tctgg
 25

<210> 53
 <211> 3753
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (184) ... (3406)

- 103 -

<400> 53
cagcagcaga agcactgcgc ggcattgcag cgatcgagcg ggaggaattt ggggcatggt 60
ggtcgccaac gccgctcgga tctagaggcc cgcacgggcc gattgggtctc cgcccgcctc 120
gtcgggtgtg gtgtcggttg cgtgtggagc cgtctcggtg ggagcagcgg ggagggagcg 180
gag atg gcg gcc aac aag ggg atg gtg gcg ggc tcg cac aac cgc aac 228
Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn
1 5 10 15
gag ttc gtc atg atc cgc cac gac ggc gat gtg ccg ggc tcg gct aag 276
Glu Phe Val Met Ile Arg His Asp Gly Asp Val Pro Gly Ser Ala Lys
20 25 30
ccc aca aag agt gcg aat gga cag gtc tgc cag att tgc ggt gac tct 324
Pro Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Ser
35 40 45
gtg ggt gtt tca gcc act ggt gat gtc ttt gtt gcc tgc aat gag tgt 372
Val Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys
50 55 60
gcc ttc cct gtc tgc cgc cca tgc tat gag tat gag cgc aag gag ggg 420
Ala Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly
65 70 75
aac caa tgc tgc ccc cag tgc aag act aga tac aag aga cag aaa ggt 468
Asn Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly
80 85 90 95
agc cct cga gtt cat ggt gat gag gat gag gaa gat gtt gat gac cta 516
Ser Pro Arg Val His Gly Asp Glu Asp Glu Glu Asp Val Asp Asp Leu
100 105 110
gac aat gaa ttc aac tac aag caa ggc agt ggg aaa ggc cca gag tgg 564
Asp Asn Glu Phe Asn Tyr Lys Gln Gly Ser Gly Lys Gly Pro Glu Trp
115 120 125
caa ctg caa gga gat gat gct gat ctg tct tca tct gct cgc cat gag 612
Gln Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Glu
130 135 140
cca cat cat cgg att cca cgc ctg aca agc ggt caa cag ata tct gga 660
Pro His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly
145 150 155
gag att cct gat gct tcc cct gac cgt cat tct atc cgc agt cca aca 708
Glu Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr
160 165 170 175
tcg agc tat gtt gat cca agc gtc cca gtt cct gtg agg att gtg gac 756
Ser Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp
180 185 190
ccc tcg aag gac ttg aat tcc tat ggg ctt aat agt gtt gac tgg aag 804
Pro Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys
195 200 205
gaa aga gtt gag agc tgg agg gtt aaa cag gac aaa aat atg atg caa 852
Glu Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Met Gln

- 104 -

210	215	220	
gtg act aat aaa tat cca gag gct aga gga gga gac atg gag ggg act			900
Val Thr Asn Lys Tyr Pro Glu Ala Arg Gly Gly Asp Met Glu Gly Thr			
225	230	235	
ggc tca aat gga gaa nat atg caa atg gtt gat gat gca cgg cta cct			948
Gly Ser Asn Gly Glu Xaa Met Gln Met Val Asp Asp Ala Arg Leu Pro			
240	245	250	255
ttg agc cgt atc gtg cca att tcc tca aac cag ctc aac ctt tac cgg			996
Leu Ser Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg			
	260	265	270
gta gtg atc att ctc cgt ctt atc atc ctg tgc ttc ttc ttc cag tat			1044
Val Val Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr			
	275	280	285
cgt gtc agt cat cca gtg cgt gat gct tat gga tta tgg cta gta tct			1092
Arg Val Ser His Pro Val Arg Asp Ala Tyr Gly Leu Trp Leu Val Ser			
	290	295	300
gtt atc tgc gag gtc tgg ttt gcc ttg tct tgg ctt cta gat cag ttc			1140
Val Ile Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe			
	305	310	315
cca aaa tgg tat cca atc aac cgt gag aca tat ctt gac agg ctt gca			1188
Pro Lys Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala			
	320	325	330
ttg agg tat gat aga gag gga gag cca tca cag ctg gct ccc att gat			1236
Leu Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp			
	340	345	350
gtc ttc gtc agt aca gtg gat cca ttg aag gaa cct cca ctg atc aca			1284
Val Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr			
	355	360	365
gcc aac act gtt ttg tcc att ctt tct gtg gat tac cct gtt gac aaa			1332
Ala Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys			
	370	375	380
gtg tca tgc tat gtt tct gat gat ggt tca gct atg ctg act ttt gag			1380
Val Ser Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu			
	385	390	395
tct ctc tca gaa acc gca gaa ttt gct aga aag tgg gtt ccc ttt tgt			1428
Ser Leu Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys			
	400	405	410
aag aag cac aat att gaa cca aga gct cca gaa ttt tac ttt gct caa			1476
Lys Lys His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln			
	420	425	430
aaa ata gat tac ctg aag gac aaa att caa cct tca ttt gtt aag gaa			1524
Lys Ile Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu			
	435	440	445

- 105 -

aga cgc gca atg aag agg gag tat gaa gaa ttc aaa gta aga atc aat	1572
Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn	
450 455 460	
gcc ctt gtt gcc aaa gca cag aaa gtg cct gaa gag ggg tgg acc atg	1620
Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met	
465 470 475	
gct gat gga act gca tgg cct ggg aat aat cct agg gac cat cct ggc	1668
Ala Asp Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly	
480 485 490 495	
atg att cag gtt ttc ttg ggg cac agt ggt ggg ctc gac act gat gga	1716
Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly	
500 505 510	
aat gag tta cca cgt ctt gtc tat gtc tct cgt gaa aag aga cca ggc	1764
Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly	
515 520 525	
ttt cag cat cac aag aag gct ggt gca atg aat gcg ctg att cgt gta	1812
Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val	
530 535 540	
tct gct gtg ctg aca aat ggt gcc tat ctt ctc aat gtg gat tgc gac	1860
Ser Ala Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp	
545 550 555	
cat tac ttc aat agc agc aaa gct ctt aga gaa gca atg tgc ttc atg	1908
His Tyr Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met	
560 565 570 575	
atg gat ccg gct cta gga agg aaa act tgt tat gta caa ttt cca cag	1956
Met Asp Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln	
580 585 590	
aga ttt gat ggc att gac ttg cac gat cga tat gct aat cgg aac ata	2004
Arg Phe Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile	
595 600 605	
gtt ttc ttt gat atc aac atg aaa ggt ctg gat ggc att cag ggt cca	2052
Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro	
610 615 620	
gtt tac gtg gga aca gga tgc tgt ttc aat aga cag gct ttg tat gga	2100
Val Tyr Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly	
625 630 635	
tac gat cct gtt ttg act gaa gct gat ctg gag cca aac att gtt att	2148
Tyr Asp Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Ile	
640 645 650 655	
aag agc tgc tgt ggt aga agg aag aaa aag aac aag agt tat atg gat	2196
Lys Ser Cys Cys Gly Arg Arg Lys Lys Lys Asn Lys Ser Tyr Met Asp	
660 665 670	
agt caa agc cgt att atg aag aga aca gaa tct tca gct ccc atc ttc	2244
Ser Gln Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe	

- 106 -

675	680	685	
aat atg gaa gac atc gaa gag ggt att gaa ggt tac gag gat gaa agg Asn Met Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg 690 695 700			2292
tca gtg ctt atg tcc cag agg aaa ttg gag aaa cgc ttt ggt cag tct Ser Val Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser 705 710 715			2340
cct att ttc att gca tcc acc ttt atg aca caa ggt ggc ata cca cct Pro Ile Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro 720 725 730 735			2388
tca aca aac cca gct tct cta cta aag gaa gct atc cat gtc atc agt Ser Thr Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser 740 745 750			2436
tgt gga tat gag gac aaa act gaa tgg gga aaa gag att ggc tgg atc Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile 755 760 765			2484
tat ggt tca gta acg gag gat att ctg act ggg ttt aaa atg cat gca Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala 770 775 780			2532
agg ggc tgg caa tca atc tac tgc atg cca cca cga cct tgt ttc aag Arg Gly Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys 785 790 795			2580
ggg tct gca cca atc aat ctt tcc gat cgt ctt aat cag gtg ctc cgt Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg 800 805 810 815			2628
tgg gct ctt ggg tca gtg gaa att ctg ctt agt aga cat tgt cct atc Trp Ala Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile 820 825 830			2676
tgg tat ggt tac aat gga cga ttg aag ctt ttg gag agg ctg gct tac Trp Tyr Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr 835 840 845			2724
atc aac act att gta tat cca atc aca tcc att ccg ctt att gcc tat Ile Asn Thr Ile Val Tyr Pro Ile Thr Ser Ile Pro Leu Ile Ala Tyr 850 855 860			2772
tgt gtg ctt ccc gct atc tgc ctc ctt acc aat aaa ttt atc att cct Cys Val Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro 865 870 875			2820
gag att agc aat tat gct ggg atg ttc ttc att ctt ctt ttc gcc tcc Glu Ile Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser 880 885 890 895			2868
att ttt gcc act ggt ata ttg gag ctt aga tgg agt ggt gtt ggc att Ile Phe Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile 900 905 910			2916

- 107 -

gaa gat tgg tgg aga aat gag cag ttt tgg gtt att ggt ggc acc tct	2964
Glu Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser	
915 920 925	
gcc cat ctc ttc gca gtg ttc cag ggt ctg ctg aaa gtg ttg gct ggg	3012
Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly	
930 935 940	
att gat acc aac ttc aca gtt acc tca aag gca tct gat gag gat ggc	3060
Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly	
945 950 955	
gac ttt gct gag cta tat gtg ttc aag tgg acc agt ttg ctc att cct	3108
Asp Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro	
960 965 970 975	
ccg acc act gtt ctt gtc att aac ctg gtc gga atg gtg gca gga att	3156
Pro Thr Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile	
980 985 990	
tct tat gcc att aac agt ggc tac caa tcc tgg ggt ccg ctc ttt gga	3204
Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly	
995 1000 1005	
aag ctg ttc ttc tcg atc tgg gtg atc ctc cat ctc tac ccc ttc ctc	3252
Lys Leu Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu	
1010 1015 1020	
aag ggt ctc atg gga agg cag aac cgc aca cca aca atc gtc att gtc	3300
Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val	
1025 1030 1035	
tgg tcc atc ctt ctt gca tct atc ttc tcc ttg ctg tgg gtg aag atc	3348
Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile	
1040 1045 1050 1055	
gat cct ttc atc tcc ccg aca cag aaa gct gct gcc ttg ggg caa tgt	3396
Asp Pro Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys	
1060 1065 1070	
ggc gtc aac t gctgatcgag acagtgactc ttatttgaag aggctcaatc	3446
Gly Val Asn	
aagatctgcc ccctcgtgta aatacctgag gaggctagat gggaattcct tttgtttag	3506
gtgaggatgg atttgcattc aagttatgcc tctgttcatt agcttcctcc gtgccggtgc	3566
tgctgcggac taagaatcac ggagcctttc taccttccat gtagcgccag ccagcagcgt	3626
aagatgtgaa ttttgaagtt ttgttatgag tgcagtttat tgttttagag taaattatca	3686
tttgtttgtg ggaactgttc acacgagcct ataatggcaa tgctgttatt taaaaaaaaa	3746
aaaaaaaa	3753
<210> 54	
<211> 1075	
<212> PRT	
<213> Zea mays	
<400> 54	
Met Ala Ala Asn Lys Gly Met Val Ala Gly Ser His Asn Arg Asn Glu	

- 108 -

```

1           5           10           15
Phe Val Met Ile Arg His Asp Gly Asp Val Pro Gly Ser Ala Lys Pro
20           25           30
Thr Lys Ser Ala Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Ser Val
35           40           45
Gly Val Ser Ala Thr Gly Asp Val Phe Val Ala Cys Asn Glu Cys Ala
50           55           60
Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Glu Gly Asn
65           70           75           80
Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser
85           90           95
Pro Arg Val His Gly Asp Glu Asp Glu Glu Asp Val Asp Asp Leu Asp
100          105          110
Asn Glu Phe Asn Tyr Lys Gln Gly Ser Gly Lys Gly Pro Glu Trp Gln
115          120          125
Leu Gln Gly Asp Asp Ala Asp Leu Ser Ser Ser Ala Arg His Glu Pro
130          135          140
His His Arg Ile Pro Arg Leu Thr Ser Gly Gln Gln Ile Ser Gly Glu
145          150          155          160
Ile Pro Asp Ala Ser Pro Asp Arg His Ser Ile Arg Ser Pro Thr Ser
165          170          175
Ser Tyr Val Asp Pro Ser Val Pro Val Pro Val Arg Ile Val Asp Pro
180          185          190
Ser Lys Asp Leu Asn Ser Tyr Gly Leu Asn Ser Val Asp Trp Lys Glu
195          200          205
Arg Val Glu Ser Trp Arg Val Lys Gln Asp Lys Asn Met Met Gln Val
210          215          220
Thr Asn Lys Tyr Pro Glu Ala Arg Gly Gly Asp Met Glu Gly Thr Gly
225          230          235          240
Ser Asn Gly Glu Xaa Met Gln Met Val Asp Asp Ala Arg Leu Pro Leu
245          250          255
Ser Arg Ile Val Pro Ile Ser Ser Asn Gln Leu Asn Leu Tyr Arg Val
260          265          270
Val Ile Ile Leu Arg Leu Ile Ile Leu Cys Phe Phe Phe Gln Tyr Arg
275          280          285
Val Ser His Pro Val Arg Asp Ala Tyr Gly Leu Trp Leu Val Ser Val
290          295          300
Ile Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe Pro
305          310          315          320
Lys Trp Tyr Pro Ile Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu
325          330          335
Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp Val
340          345          350
Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala
355          360          365
Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val
370          375          380
Ser Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser
385          390          395          400
Leu Ser Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys
405          410          415
Lys His Asn Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln Lys
420          425          430
Ile Asp Tyr Leu Lys Asp Lys Ile Gln Pro Ser Phe Val Lys Glu Arg
435          440          445
Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala
450          455          460
Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Ala

```

- 109 -

465		470		475		480
Asp Gly Thr Ala Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met						
	485		490		495	
Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn						
	500		505		510	
Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe						
	515		520		525	
Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser						
	530		535		540	
Ala Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His						
545	550		555		560	
Tyr Phe Asn Ser Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met						
	565		570		575	
Asp Pro Ala Leu Gly Arg Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg						
	580		585		590	
Phe Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val						
	595		600		605	
Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val						
	610		615		620	
Tyr Val Gly Thr Gly Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr						
625	630		635		640	
Asp Pro Val Leu Thr Glu Ala Asp Leu Glu Pro Asn Ile Val Ile Lys						
	645		650		655	
Ser Cys Cys Gly Arg Arg Lys Lys Lys Asn Lys Ser Tyr Met Asp Ser						
	660		665		670	
Gln Ser Arg Ile Met Lys Arg Thr Glu Ser Ser Ala Pro Ile Phe Asn						
	675		680		685	
Met Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Glu Asp Glu Arg Ser						
	690		695		700	
Val Leu Met Ser Gln Arg Lys Leu Glu Lys Arg Phe Gly Gln Ser Pro						
705	710		715		720	
Ile Phe Ile Ala Ser Thr Phe Met Thr Gln Gly Gly Ile Pro Pro Ser						
	725		730		735	
Thr Asn Pro Ala Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys						
	740		745		750	
Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr						
	755		760		765	
Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg						
	770		775		780	
Gly Trp Gln Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly						
785	790		795		800	
Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp						
	805		810		815	
Ala Leu Gly Ser Val Glu Ile Leu Leu Ser Arg His Cys Pro Ile Trp						
	820		825		830	
Tyr Gly Tyr Asn Gly Arg Leu Lys Leu Leu Glu Arg Leu Ala Tyr Ile						
	835		840		845	
Asn Thr Ile Val Tyr Pro Ile Thr Ser Ile Pro Leu Ile Ala Tyr Cys						
	850		855		860	
Val Leu Pro Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu						
865	870		875		880	
Ile Ser Asn Tyr Ala Gly Met Phe Phe Ile Leu Leu Phe Ala Ser Ile						
	885		890		895	
Phe Ala Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu						
	900		905		910	
Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala						
	915		920		925	
His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile						

- 110 -

930	935	940
Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp		
945	950	955
Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro		960
	965	970
Thr Thr Val Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser		975
	980	985
Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys		990
	995	1000
Leu Phe Phe Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys		1005
	1010	1015
Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp		1020
1025	1030	1035
Ser Ile Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp		1040
	1045	1050
Pro Phe Ile Ser Pro Thr Gln Lys Ala Ala Ala Leu Gly Gln Cys Gly		1055
	1060	1065
Val Asn Cys		1070
1075		

<210> 55
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 55
 atggcggcca acaaggggat ggtgg
 25

<210> 56
 <211> 25
 <212> DNA
 <213> Zea mays

<400> 56
 tcagcagttg acgccacatt gcccc
 25

<210> 57
 <211> 3704
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (272) ... (3497)

<400> 57	
gtcgaccac ggttcgggc ggttcgggc cctttttccc ctccccctc cgtcgccgcc	60
tcgagcgagc tccaccactt gctcctgccc gaggtgaaca ctgggttagg gccactgcca	120
cgcgtgggct gcctctgctt ctgcctctcc cgccagcgcg cgagcccggg ggcgattcgg	180
cgccggcagc cgggagggga agccgaggaa tgcggtgagt cggcgggggt ccggcggttg	240
tgaactcgtg gagggctcgg attggtgcgc c atg gac ggc ggc gac gcc acg	292
Met Asp Gly Gly Asp Ala Thr	
1 5	

aat tcg ggg aag cat gtg gcc ggg cag gtg tgc cag atc tgc ggc gac	340
Asn Ser Gly Lys His Val Ala Gly Gln Val Cys Gln Ile Cys Gly Asp	

- 111 -

10	15	20	
ggc gtg ggc acc gcg gcg gac ggc gac ctc ttc acc gcc tgc gac gtc Gly Val Gly Thr Ala Ala Asp Gly Asp Leu Phe Thr Ala Cys Asp Val 25 30 35			388
tgc ggc ttc ccc gtg tgc cgc cca tgc tac gag tac gag cgc aag gac Cys Gly Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Asp 40 45 50 55			436
ggc acc cag gcg tgc ccg cag tgc aag act aag tac aag cgc cac aaa Gly Thr Gln Ala Cys Pro Gln Cys Lys Thr Lys Tyr Lys Arg His Lys 60 65 70			484
ggg agc cca cca gta cac ggt gag gaa aat gag gat gtg gat gct gac Gly Ser Pro Pro Val His Gly Glu Glu Asn Glu Asp Val Asp Ala Asp 75 80 85			532
gat gtg agt gac tac aac tac caa gca tct ggc aac cag gat cag aag Asp Val Ser Asp Tyr Asn Tyr Gln Ala Ser Gly Asn Gln Asp Gln Lys 90 95 100			580
caa aag att gct gag aga atg ctc act tgg cgg aca aac tca cgt ggc Gln Lys Ile Ala Glu Arg Met Leu Thr Trp Arg Thr Asn Ser Arg Gly 105 110 115			628
agt gat att ggc ctg gct aag tat gac agc ggt gaa att ggg cat ggg Ser Asp Ile Gly Leu Ala Lys Tyr Asp Ser Gly Glu Ile Gly His Gly 120 125 130 135			676
aag tat gac agt ggt gag atc cct cgt gga tat atc ccg tca cta act Lys Tyr Asp Ser Gly Glu Ile Pro Arg Gly Tyr Ile Pro Ser Leu Thr 140 145 150			724
cat agc cag atc tca gga gag att cct gga gct tcc cct gat cat atg His Ser Gln Ile Ser Gly Glu Ile Pro Gly Ala Ser Pro Asp His Met 155 160 165			772
atg tct cct gtt ggg aac att ggc agg cgt gga cat caa ttt cct tat Met Ser Pro Val Gly Asn Ile Gly Arg Arg Gly His Gln Phe Pro Tyr 170 175 180			820
gta aat cat tct cca aac cca tcg agg gag ttc tcc ggt agc ctt ggc Val Asn His Ser Pro Asn Pro Ser Arg Glu Phe Ser Gly Ser Leu Gly 185 190 195			868
aat gtt gca tgg aaa gag agg gtg gat gga tgg aaa atg aag gat aaa Asn Val Ala Trp Lys Glu Arg Val Asp Gly Trp Lys Met Lys Asp Lys 200 205 210 215			916
ggg gca att cct atg acc aat gga aca agc att gct cca tca gaa ggg Gly Ala Ile Pro Met Thr Asn Gly Thr Ser Ile Ala Pro Ser Glu Gly 220 225 230			964
cgt gga gtt gct gat att gat gct tct act gat tat aac atg gaa gat Arg Gly Val Ala Asp Ile Asp Ala Ser Thr Asp Tyr Asn Met Glu Asp 235 240 245			1012

- 112 -

gcc tta ctg aat gat gaa act cgg caa cct cta tct aga aaa gtg cca	1060
Ala Leu Leu Asn Asp Glu Thr Arg Gln Pro Leu Ser Arg Lys Val Pro	
250 255 260	
att cct tca tcc aga ata aat ccg tac aga atg gtc att gtg cta cgt	1108
Ile Pro Ser Ser Arg Ile Asn Pro Tyr Arg Met Val Ile Val Leu Arg	
265 270 275	
ttg gct gtt cta tgc ata ttc ttg cgc tac cgt atc aca cat cct gtg	1156
Leu Ala Val Leu Cys Ile Phe Leu Arg Tyr Arg Ile Thr His Pro Val	
280 285 290 295	
aac aat gca tat cca ctg tgg ctt tta tcc gtc ata tgt gag atc tgg	1204
Asn Asn Ala Tyr Pro Leu Trp Leu Leu Ser Val Ile Cys Glu Ile Trp	
300 305 310	
ttt gct ttg tcc tgg att ttg gat cag ttc cca aag tgg tcc cca atc	1252
Phe Ala Leu Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Ser Pro Ile	
315 320 325	
aac cgt gaa aca tac ctt gat aga ctg gct tta agg tat gac cga gaa	1300
Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ala Leu Arg Tyr Asp Arg Glu	
330 335 340	
ggg gaa cca tct caa tta gct cct gtt gat att ttt gtc agt act gtg	1348
Gly Glu Pro Ser Gln Leu Ala Pro Val Asp Ile Phe Val Ser Thr Val	
345 350 355	
gat cca atg aag gag cct cct ctt gtc act gca aat act gtg ctt tcc	1396
Asp Pro Met Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val Leu Ser	
360 365 370 375	
atc ctt gct gtc gat tat ccg gtt gac aag gta tct tgc tat gtt tgc	1444
Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser Cys Tyr Val Ser	
380 385 390	
gat gat gga gct gct atg ctg act ttt gat gct ctc tct gaa act tca	1492
Asp Asp Gly Ala Ala Met Leu Thr Phe Asp Ala Leu Ser Glu Thr Ser	
395 400 405	
gag ttt gct aga aaa tgg gtt ccg ttc tgt aag aag tac aac ata gag	1540
Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys Tyr Asn Ile Glu	
410 415 420	
cct ang gcc ccg gaa tgg tac ttt gct cag aaa att gat tac ttg aaa	1588
Pro Xaa Ala Pro Glu Trp Tyr Phe Ala Gln Lys Ile Asp Tyr Leu Lys	
425 430 435	
gac aaa gtt caa acc tca ttt gtg aaa gaa cgc cgg gcc atg aag aga	1636
Asp Lys Val Gln Thr Ser Phe Val Lys Glu Arg Arg Ala Met Lys Arg	
440 445 450 455	
gaa tat gaa gaa ttc aaa gtt cgt atc aat ggt ctt gta gcc aag gca	1684
Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Gly Leu Val Ala Lys Ala	
460 465 470	
caa aaa gtt ccc gag gag gga tgg atc atg caa gat ggt aca cct tgg	1732
Gln Lys Val Pro Glu Glu Gly Trp Ile Met Gln Asp Gly Thr Pro Trp	

- 113 -

475	480	485	
cct ggg aac aat act agg gac cat	cct gga atg att cag gtt ttc ctg		1780
Pro Gly Asn Asn Thr Arg Asp His	Pro Gly Met Ile Gln Val Phe Leu		
490	495	500	
ggg cac agt gga ggg ctt gac gtt gaa ggc aat gaa ctt cct cgt ttg			1828
Gly His Ser Gly Gly Leu Asp Val Glu Gly Asn Glu Leu Pro Arg Leu			
505	510	515	
gtt tat gtg tct cgt gaa aaa cgt cct gga ttc caa cat cac aag aag			1876
Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln His His Lys Lys			
520	525	530	535
gct ggt gcc atg aat gca ctt gtt cgt gta tca gct gtc ctt act aat			1924
Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn			
540	545	550	
ggg caa tac atg ttg aat ctt gat tgt gac cac tac atc aat aat agc			1972
Gly Gln Tyr Met Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser			
555	560	565	
aag gct ctt cga gaa gct atg tgc ttc ctt atg gac cca aac cta gga			2020
Lys Ala Leu Arg Glu Ala Met Cys Phe Leu Met Asp Pro Asn Leu Gly			
570	575	580	
agg aat gtc tgt tat gtc caa ttt cct cag agg ttt gat ggt att gat			2068
Arg Asn Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp			
585	590	595	
agg aat gac cga tat gca aac agg aac act gtg ttt ttc gat att aac			2116
Arg Asn Asp Arg Tyr Ala Asn Arg Asn Thr Val Phe Phe Asp Ile Asn			
600	605	610	615
ttg aga ggt ctt gac ggc att caa ggg cca gtt tat gtg gga act ggt			2164
Leu Arg Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr Val Gly Thr Gly			
620	625	630	
tgt gtg ttt aac aga acg gcc tta tat ggt tat gag cct cca gtc aag			2212
Cys Val Phe Asn Arg Thr Ala Leu Tyr Gly Tyr Glu Pro Pro Val Lys			
635	640	645	
aaa aaa aag cca ggc ttc ttc tct tcg ctt tgt ggg gga agg aaa aag			2260
Lys Lys Lys Pro Gly Phe Phe Ser Ser Leu Cys Gly Gly Arg Lys Lys			
650	655	660	
acg tca aaa tct aag aag agc tcg gaa aag aag aag tca cat aga cac			2308
Thr Ser Lys Ser Lys Lys Ser Ser Glu Lys Lys Lys Ser His Arg His			
665	670	675	
gca gac agt tct gta cca gta ttt aat ctc gaa gat ata gag gaa ggg			2356
Ala Asp Ser Ser Val Pro Val Phe Asn Leu Glu Asp Ile Glu Glu Gly			
680	685	690	695
att gaa ggt tct cag ttt gat gat gag aaa tcg ctg att atg tct caa			2404
Ile Glu Gly Ser Gln Phe Asp Asp Glu Lys Ser Leu Ile Met Ser Gln			
700	705	710	

- 114 -

atg agc ttg gag aag aga ttt ggc cag tcc agt gtt ttt gta gcc tct	2452
Met Ser Leu Glu Lys Arg Phe Gly Gln Ser Ser Val Phe Val Ala Ser	
715 720 725	
act ctg atg gaa tat ggt ggt gtt cca caa tct gca act cca gag tct	2500
Thr Leu Met Glu Tyr Gly Gly Val Pro Gln Ser Ala Thr Pro Glu Ser	
730 735 740	
ctt ctg aaa gaa gct att cat gtc atc agc tgt ggc tat gag gac aaa	2548
Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys	
745 750 755	
act gac tgg gga act gag att ggg tgg atc tat ggt tct gtt aca gaa	2596
Thr Asp Trp Gly Thr Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu	
760 765 770 775	
gac att ctc acc gga ttc aag atg cat gct cga ggc tgg cga tca atc	2644
Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Arg Ser Ile	
780 785 790	
tac tgc atg cct aag cga cca gct ttc aag gga tct gct cct atc aac	2692
Tyr Cys Met Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn	
795 800 805	
ctt tcg gat cgt ttg aat caa gtg ctt cgg tgg gct ctt ggt tcc att	2740
Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly Ser Ile	
810 815 820	
gaa att ctt ttc agc agg cat tgt ccc ata tgg tat ggc tat gga ggc	2788
Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Gly Tyr Gly Gly	
825 830 835	
cgg ctt aaa ttc ctg gag aga ttt gct tat atc aac aca aca att tat	2836
Arg Leu Lys Phe Leu Glu Arg Phe Ala Tyr Ile Asn Thr Thr Ile Tyr	
840 845 850 855	
cca ctc aca tca atc ccg ctc ctc ctg tac tgc ata ttg cca gca gtt	2884
Pro Leu Thr Ser Ile Pro Leu Leu Leu Tyr Cys Ile Leu Pro Ala Val	
860 865 870	
tgt ctt ctc act ggg aag ttc atc atc cca aag att agt aac cta gag	2932
Cys Leu Leu Thr Gly Lys Phe Ile Ile Pro Lys Ile Ser Asn Leu Glu	
875 880 885	
agt gtt tgg ttt ata tcg ctc ttt atc tca atc ttt gcc act ggt atc	2980
Ser Val Trp Phe Ile Ser Leu Phe Ile Ser Ile Phe Ala Thr Gly Ile	
890 895 900	
ctt gag atg agg tgg agt ggt gtt ggc att gat gaa tgg tgg agg aac	3028
Leu Glu Met Arg Trp Ser Gly Val Gly Ile Asp Glu Trp Trp Arg Asn	
905 910 915	
gag cag ttc tgg gtc att ggt ggt att tct gcg cat tta ttt gcc gtc	3076
Glu Gln Phe Trp Val Ile Gly Gly Ile Ser Ala His Leu Phe Ala Val	
920 925 930 935	
ttc cag ggt ctc ctg aag gtg ctt gct ggt atc gac acg agc ttc act	3124
Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Ser Phe Thr	

- 115 -

940	945	950	
gtc acc tct aag gcc act gac gaa gaa ggt gat ttt gcc gag ctc tac			3172
Val Thr Ser Lys Ala Thr Asp Glu Glu Gly Asp Phe Ala Glu Leu Tyr			
955	960	965	
atg ttc aag tgg aca acg ctt ctg atc cca cca acc act att ttg atc			3220
Met Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Ile Leu Ile			
970	975	980	
atc aac ctg gtc ggc gtg gtc gct ggc att tcc tac gca atc aat agc			3268
Ile Asn Leu Val Gly Val Val Ala Gly Ile Ser Tyr Ala Ile Asn Ser			
985	990	995	
ggt tac cag tca tgg gga cct ctt ttc ggg aag ctc ttc ttt gcg ttc			3316
Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe			
1000	1005	1010	1015
tgg gtg att gtc cac ctg tac ccc ttc ctc aag ggc ctc atg ggg aag			3364
Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Lys			
1020	1025	1030	
cag aac cgc acg ccg acc att gtc gtt gtc tgg gct atc ctc ctt gcg			3412
Gln Asn Arg Thr Pro Thr Ile Val Val Val Trp Ala Ile Leu Leu Ala			
1035	1040	1045	
tcg atc ttt tcc ctg atg tgg gtt cgt atc gat cca ttc acc acc cgg			3460
Ser Ile Phe Ser Leu Met Trp Val Arg Ile Asp Pro Phe Thr Thr Arg			
1050	1055	1060	
gtc act ggc cct gat atc gcg aaa tgt ggc atc aac t gctaggatga			3507
Val Thr Gly Pro Asp Ile Ala Lys Cys Gly Ile Asn			
1065	1070	1075	
gctgaagata gttaaagagt ggaactagac gcattgtgca tcgtaagtta tcagtgggtg 3567			
gctcttttta tagtatggta ggaacttggt cgggagacgt taattacata tgctatatgt 3627			
acctccgctg gtcttttatcc gtaagttaat atatatactg ctttgagaat taaaaaaaaa 3687			
aaaaaaaggg cggccgc 3704			

<210> 58

<211> 1076

<212> PRT

<213> Zea mays

<400> 58

Met Asp Gly Gly Asp Ala Thr Asn Ser Gly Lys His Val Ala Gly Gln			
1	5	10	15
Val Cys Gln Ile Cys Gly Asp Gly Val Gly Thr Ala Ala Asp Gly Asp			
20	25	30	
Leu Phe Thr Ala Cys Asp Val Cys Gly Phe Pro Val Cys Arg Pro Cys			
35	40	45	
Tyr Glu Tyr Glu Arg Lys Asp Gly Thr Gln Ala Cys Pro Gln Cys Lys			
50	55	60	
Thr Lys Tyr Lys Arg His Lys Gly Ser Pro Pro Val His Gly Glu Glu			
65	70	75	80
Asn Glu Asp Val Asp Ala Asp Asp Val Ser Asp Tyr Asn Tyr Gln Ala			
85	90	95	
Ser Gly Asn Gln Asp Gln Lys Gln Lys Ile Ala Glu Arg Met Leu Thr			

				100						105				110		
Trp	Arg	Thr	Asn	Ser	Arg	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Lys	Tyr	Asp	
		115					120					125				
Ser	Gly	Glu	Ile	Gly	His	Gly	Lys	Tyr	Asp	Ser	Gly	Glu	Ile	Pro	Arg	
	130					135					140					
Gly	Tyr	Ile	Pro	Ser	Leu	Thr	His	Ser	Gln	Ile	Ser	Gly	Glu	Ile	Pro	
145					150					155					160	
Gly	Ala	Ser	Pro	Asp	His	Met	Met	Ser	Pro	Val	Gly	Asn	Ile	Gly	Arg	
				165					170					175		
Arg	Gly	His	Gln	Phe	Pro	Tyr	Val	Asn	His	Ser	Pro	Asn	Pro	Ser	Arg	
		180						185					190			
Glu	Phe	Ser	Gly	Ser	Leu	Gly	Asn	Val	Ala	Trp	Lys	Glu	Arg	Val	Asp	
	195					200					205					
Gly	Trp	Lys	Met	Lys	Asp	Lys	Gly	Ala	Ile	Pro	Met	Thr	Asn	Gly	Thr	
	210					215					220					
Ser	Ile	Ala	Pro	Ser	Glu	Gly	Arg	Gly	Val	Ala	Asp	Ile	Asp	Ala	Ser	
225					230					235					240	
Thr	Asp	Tyr	Asn	Met	Glu	Asp	Ala	Leu	Leu	Asn	Asp	Glu	Thr	Arg	Gln	
				245					250					255		
Pro	Leu	Ser	Arg	Lys	Val	Pro	Ile	Pro	Ser	Ser	Arg	Ile	Asn	Pro	Tyr	
			260					265					270			
Arg	Met	Val	Ile	Val	Leu	Arg	Leu	Ala	Val	Leu	Cys	Ile	Phe	Leu	Arg	
	275					280					285					
Tyr	Arg	Ile	Thr	His	Pro	Val	Asn	Asn	Ala	Tyr	Pro	Leu	Trp	Leu	Leu	
	290				295					300						
Ser	Val	Ile	Cys	Glu	Ile	Trp	Phe	Ala	Leu	Ser	Trp	Ile	Leu	Asp	Gln	
305				310						315					320	
Phe	Pro	Lys	Trp	Ser	Pro	Ile	Asn	Arg	Glu	Thr	Tyr	Leu	Asp	Arg	Leu	
				325				330					335			
Ala	Leu	Arg	Tyr	Asp	Arg	Glu	Gly	Glu	Pro	Ser	Gln	Leu	Ala	Pro	Val	
			340					345					350			
Asp	Ile	Phe	Val	Ser	Thr	Val	Asp	Pro	Met	Lys	Glu	Pro	Pro	Leu	Val	
	355					360					365					
Thr	Ala	Asn	Thr	Val	Leu	Ser	Ile	Leu	Ala	Val	Asp	Tyr	Pro	Val	Asp	
	370				375						380					
Lys	Val	Ser	Cys	Tyr	Val	Ser	Asp	Asp	Gly	Ala	Ala	Met	Leu	Thr	Phe	
385				390						395					400	
Asp	Ala	Leu	Ser	Glu	Thr	Ser	Glu	Phe	Ala	Arg	Lys	Trp	Val	Pro	Phe	
				405					410					415		
Cys	Lys	Lys	Tyr	Asn	Ile	Glu	Pro	Xaa	Ala	Pro	Glu	Trp	Tyr	Phe	Ala	
			420					425					430			
Gln	Lys	Ile	Asp	Tyr	Leu	Lys	Asp	Lys	Val	Gln	Thr	Ser	Phe	Val	Lys	
		435					44									

Leu	Met	Asp	Pro	Asn	Leu	Gly	Arg	Asn	Val	Cys	Tyr	Val	Gln	Phe	Pro
			580					585					590		
Gln	Arg	Phe	Asp	Gly	Ile	Asp	Arg	Asn	Asp	Arg	Tyr	Ala	Asn	Arg	Asn
		595					600					605			
Thr	Val	Phe	Phe	Asp	Ile	Asn	Leu	Arg	Gly	Leu	Asp	Gly	Ile	Gln	Gly
		610				615					620				
Pro	Val	Tyr	Val	Gly	Thr	Gly	Cys	Val	Phe	Asn	Arg	Thr	Ala	Leu	Tyr
625					630					635					640
Gly	Tyr	Glu	Pro	Pro	Val	Lys	Lys	Lys	Lys	Pro	Gly	Phe	Phe	Ser	Ser
				645					650					655	
Leu	Cys	Gly	Gly	Arg	Lys	Lys	Thr	Ser	Lys	Ser	Lys	Lys	Ser	Ser	Glu
			660					665					670		
Lys	Lys	Lys	Ser	His	Arg	His	Ala	Asp	Ser	Ser	Val	Pro	Val	Phe	Asn
		675					680					685			
Leu	Glu	Asp	Ile	Glu	Glu	Gly	Ile	Glu	Gly	Ser	Gln	Phe	Asp	Asp	Glu
						695					700				
Lys	Ser	Leu	Ile	Met	Ser	Gln	Met	Ser	Leu	Glu	Lys	Arg	Phe	Gly	Gln
705						710				715					720
Ser	Ser	Val	Phe	Val	Ala	Ser	Thr	Leu	Met	Glu	Tyr	Gly	Gly	Val	Pro
				725					730					735	
Gln	Ser	Ala	Thr	Pro	Glu	Ser	Leu	Leu	Lys	Glu	Ala	Ile	His	Val	Ile
			740					745					750		
Ser	Cys	Gly	Tyr	Glu	Asp	Lys	Thr	Asp	Trp	Gly	Thr	Glu	Ile	Gly	Trp
		755					760					765			
Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met	His
		770				775					780				
Ala	Arg	Gly	Trp	Arg	Ser	Ile	Tyr	Cys	Met	Pro	Lys	Arg	Pro	Ala	Phe
785						790				795					800
Lys	Gly	Ser	Ala	Pro	Ile	Asn	Leu	Ser	Asp	Arg	Leu	Asn	Gln	Val	Leu
				805					810					815	
Arg	Trp	Ala	Leu	Gly	Ser	Ile	Glu	Ile	Leu	Phe	Ser	Arg	His	Cys	Pro
			820					825					830		
Ile	Trp	Tyr	Gly	Tyr	Gly	Gly	Arg	Leu	Lys	Phe	Leu	Glu	Arg	Phe	Ala
		835					840					845			
Tyr	Ile	Asn	Thr	Thr	Ile	Tyr	Pro	Leu	Thr	Ser	Ile	Pro	Leu	Leu	Leu
		850				855					860				
Tyr	Cys	Ile	Leu	Pro	Ala	Val	Cys	Leu	Leu	Thr	Gly	Lys	Phe	Ile	Ile
865					870					875					880
Pro	Lys	Ile	Ser	Asn	Leu	Glu	Ser	Val	Trp	Phe	Ile	Ser	Leu	Phe	Ile
				885					890					895	
Ser	Ile	Phe	Ala	Thr	Gly	Ile	Leu	Glu	Met	Arg	Trp	Ser	Gly	Val	Gly
			900					905					910		
Ile	Asp	Glu	Trp	Trp	Arg	Asn	Glu								

- 118 -

1025 1030 1035 1040
Val Trp Ala Ile Leu Leu Ala Ser Ile Phe Ser Leu Met Trp Val Arg
 1045 1050 1055
Ile Asp Pro Phe Thr Thr Arg Val Thr Gly Pro Asp Ile Ala Lys Cys
 1060 1065 1070
Gly Ile Asn Cys
 1075

<210> 59
<211> 25
<212> DNA
<213> Zea mays

<400> 59
atggacggcg gcgacgccac gaatt
25

<210> 60
<211> 25
<212> DNA
<213> Zea mays

<400> 60
ctagcagttg atgccacatt tcgcg
25
119

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/54, 9/10, 5/10, 15/82	A3	(11) International Publication Number: WO 00/09706 (43) International Publication Date: 24 February 2000 (24.02.00)
(21) International Application Number: PCT/US99/18760 (22) International Filing Date: 16 August 1999 (16.08.99) (30) Priority Data: 60/096,822 17 August 1998 (17.08.98) US (71) Applicant (for all designated States except US): PIONEER HI-BRED INTERNATIONAL, INC. [US/US]; 800 Capital Square, 400 Locust Street, Des Moines, IA 50309 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): DHUGGA, Kanwarpal, S. [US/US]; 8320 Barnham Drive, Johnston, IA 50131 (US). HELENTJARIS, Timothy, G. [US/US]; 2960 N.W. 73rd Lane, Ankeny, IA 50021 (US). BOWEN, Benjamin, A. [GB/US]; 7027 Buckingham Boulevard, Berkeley, CA 94705 (US). WANG, Xun [CN/US]; 12524 Caminito Vista Soledad, San Diego, CA 92130 (US). (74) Agents: BLAIR, Debra, L. et al.; 7100 N.W. 62nd Avenue, Darwin Building, Johnston, IA 50131-1000 (US).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> (88) Date of publication of the international search report: 16 November 2000 (16.11.00)
(54) Title: MAIZE CELLULOSE SYNTHASES AND USES THEREOF (57) Abstract <p>The invention provides isolated cellulose synthase nucleic acids and their encoded proteins. The present invention provides methods and compositions relating to altering cellulose synthase concentration and/or composition of plants. The invention further provides recombinant expression cassettes, host cells, and transgenic plants.</p>		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/18760

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/54 C12N9/10 C12N5/10 C12N15/82

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

STRAND, EPO-Internal, WPI Data, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
1 X	WO 98 00549 A (WILLIAMSON RICHARD EDWARD ;PENG LIANGCAI (AU); ARIOLI ANTONIO (AU)) 8 January 1998 (1998-01-08) abstract page 4, line 10 - line 14 page 7, line 19 - line 29 page 8, line 16 - line 21 page 11, line 6 - line 12 page 17, line 4 - line 19 page 24, line 15 - line 18 page 28, line 15 - line 21 ---	1-15
1 A	WO 98 18949 A (CALGENE INC ;PEAR JULIE R (US); STALKER DAVID M (US); DELMER DEBOR) 7 May 1998 (1998-05-07) cited in the application abstract page 7, line 14 -page 9, line 25 --- -/--	1-15

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

22 June 2000

Date of making of the international search report

14. 7. 00

Name and mailing address of the ISA

European Patent Office, P.B. 5918 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Ceder, O

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/18760

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>ARIOLI ET AL.: "Molecular analysis of cellulose biosynthesis in Arabidopsis" EMBL SEQUENCE DATABASE, 1 June 1998 (1998-06-01), XP002125688 HEIDELBERG DE Ac 048947 the whole document</p>	15
A	<p>-& ARIOLI ET AL.: "Molecular analysis of cellulose biosynthesis in Arabidopsis" EMBL SEQUENCE DATABASE, 3 February 1998 (1998-02-03), XP002125689 HEIDELBERG DE AC AF027174 the whole document</p>	1
X	<p>-& ARIOLI ET AL.: "Molecular analysis of cellulose biosynthesis in Arabidopsis" EMBL SEQUENCE DATABASE, 1 June 1998 (1998-06-01), XP002140697 HEIDELBERG DE Ac 048948 the whole document</p>	15
X	<p>-& ARIOLI ET AL.: "Molecular analysis of cellulose biosynthesis in Arabidopsis" EMBL SEQUENCE DATABASE, 20 January 1998 (1998-01-20), XP002140698 HEIDELBERG DE Ac AF030052 the whole document</p>	1
X	<p>-& ARIOLI ET AL.: "Molecular analysis of cellulose biosynthesis in Arabidopsis" EMBL SEQUENCE DATABASE, 1 June 1998 (1998-06-01), XP002140699 HEIDELBERG DE Ac 048946 the whole document</p>	15
A	<p>-& ARIOLI ET AL.: "Molecular analysis of cellulose biosynthesis in Arabidopsis" EMBL SEQUENCE DATABASE, 3 February 1998 (1998-02-03), XP002140700 HEIDELBERG DE Ac AF027173 the whole document</p>	15
X	<p>-& ARIOLI ET AL.: "Molecular analysis of cellulose biosynthesis in Arabidopsis" SCIENCE, vol. 279, no. 5351, 30 January 1998 (1998-01-30), pages 717-720, XP002124283</p>	15
A	<p>abstract; figure 3</p>	1
	<p>---</p> <p>-/--</p>	

INTERNATIONAL SEARCH REPORT

Intern. Patent Application No

PCT/US 99/18760

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>WU ET AL.: "Cellulose synthase" EMBL SEQUENCE DATABASE, 1 August 1998 (1998-08-01), XP002140701 HEIDELBERG DE Ac 065338 the whole document</p> <p style="text-align: center;">----</p>	15
A	<p>PEAR J R ET AL: "HIGHER PLANTS CONTAIN HOMOLOGS OF THE BACTERIAL CELA GENES ENCODING THE CATALYTIC SUBUNIT OF CELLULOSE SYNTHASE" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, US, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, vol. 93, page 12637-12642 XP002061424 ISSN: 0027-8424</p> <p style="text-align: center;">----</p>	
A	<p>AMOR Y ET AL: "EVIDENCE FOR A CYCLIC DIGUANYLIC ACID-DEPENDENT CELLULOSE SYNTHASE IN PLANTS" PLANT CELL, US, AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS, ROCKVILLE, MD, vol. 3, page 989-995 XP002061420 ISSN: 1040-4651</p> <p style="text-align: center;">----</p>	
A	<p>US 5 723 764 A (SINGLETERY GEORGE WILLIAM ET AL) 3 March 1998 (1998-03-03) abstract; claims</p> <p style="text-align: center;">----</p>	2-12
E	<p>WO 00 04166 A (THORPE ET AL.) 27 January 2000 (2000-01-27) abstract; claims</p> <p style="text-align: center;">-----</p>	1-15

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 99/18760

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

As a result of the prior review under R. 40.2(e) PCT,
no additional fees are to be refunded.

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1-15 all partly (inventions 1,2,3,4,5,7 and 15 searched)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☒ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1: 1-15 all partial

An isolated nucleic acid selected from the groups as defined in claim 1 and uses of said nucleic acid, and a protein selected from the groups as defined in claim 15, where the nucleic acid sequence is SEQ ID NO 1 and the protein sequence is SEQ ID NO 2.

2. Claims: Inventions 2-15: Claims 1-15 all partial

Idem as subject 1 but limited to each of the nucleic acid sequences as in SEQ ID NOS 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, and 57 and corresponding protein sequences SEQ ID NOS 6, 10, 14, 18, 22, 26, 30, 34, 42, 46, 50, 54, and 58, where invention 2 is limited to SEQ ID NOS 5 and 6, invention 3 is limited to SEQ ID NOS 9 and 10,, invention 15 is limited to SEQ ID NOS 57 and 58.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 99/18760

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9800549 A	08-01-1998	AU 3160397 A CA 2259126 A EP 0956353 A	21-01-1998 08-01-1998 17-11-1999
WO 9818949 A	07-05-1998	AU 5092398 A BR 9712457 A EP 0938573 A	22-05-1998 19-10-1999 01-09-1999
US 5723764 A	03-03-1998	NONE	
WO 0004166 A	27-01-2000	AU 5100199 A	07-02-2000